

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2003, 20:07:47 ; Search time 42 seconds
(without alignments)
1067.014 Million cell updates/sec

Title: US-09-996-223-1
Perfect score: 2436
Sequence: 1 MALTTAAARLGTGNASCLV.....ERPKSMTEGIMKFDVDSKSG 466

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 1008 summaries

Database :

1: PIR.76:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----------|--------------------|
| 1 | 2339 | 96.0 | 464 | 1 YKPG | citrate (s1)-synth |
| 2 | 1693 | 69.5 | 468 | 2 S42370 | citrate (s1)-synth |
| 3 | 1519 | 62.4 | 473 | 2 T39028 | citrate synthase P |
| 4 | 1501.5 | 61.6 | 469 | 2 T49379 | citrate synthase |
| 5 | 1499.5 | 61.6 | 479 | 1 YKBY | citrate (s1)-synth |
| 6 | 1498.5 | 61.5 | 474 | 2 T02390 | citrate (s1)-synth |
| 7 | 1495.5 | 61.4 | 469 | 2 S41563 | citrate (s1)-synth |
| 8 | 1473.5 | 60.5 | 433 | 2 T47834 | citrate synthase-1 |
| 9 | 1425 | 58.5 | 460 | 1 YKBYC | citrate (s1)-synth |
| 10 | 1349 | 55.4 | 471 | 2 S44316 | citrate (s1)-synth |
| 11 | 1219 | 50.0 | 462 | 2 JCS625 | 14-nm filament pro |
| 12 | 1157.5 | 47.5 | 472 | 1 YKMDM | citrate (s1)-synth |
| 13 | 1108.5 | 45.5 | 339 | 2 T09334 | citrate (s1)-synth |
| 14 | 1063.5 | 43.7 | 486 | 2 S52814 | citrate (s1)-synth |
| 15 | 356 | 14.6 | 437 | 2 I40717 | citrate (s1)-synth |
| 16 | 351 | 14.4 | 436 | 1 YKOPC | citrate (s1)-synth |
| 17 | 346 | 14.2 | 397 | 2 S74344 | citrate synthase 9 |
| 18 | 345.5 | 14.2 | 427 | 2 B81139 | probable citrate l |
| 19 | 339.5 | 13.9 | 514 | 2 T49158 | citrate synthase-1 |
| 20 | 338 | 13.9 | 428 | 1 YKPSA | citrate (s1)-synth |
| 21 | 338 | 13.9 | 509 | 2 B83448 | citrate synthase P |
| 22 | 338 | 13.9 | 509 | 2 C84858 | probable citrate s |
| 23 | 332.5 | 13.6 | 431 | 2 T45353 | citrate synthase l |
| 24 | 331.5 | 13.6 | 431 | 2 T45353 | citrate synthase l |
| 25 | 327.5 | 13.4 | 430 | 2 J01392 | citrate (s1)-synth |
| 26 | 327.5 | 13.4 | 435 | 2 D97863 | citrate (s1)-synth |
| 27 | 324.5 | 13.3 | 411 | 2 A75479 | citrate synthase - |
| 28 | 324 | 13.3 | 426 | 2 E87485 | citrate synthase l |
| 29 | 322.5 | 13.2 | 372 | 2 H84044 | citrate synthase l |

| | | | | | |
|----|-------|------|-----|----------|--------------------|
| 30 | 322.5 | 13.2 | 516 | 2 S53007 | citrate synthase - |
| 31 | 320 | 13.1 | 441 | 2 F86708 | citrate (s1)-synth |
| 32 | 318 | 13.1 | 378 | 2 AF1834 | citrate synthase l |
| 33 | 315.5 | 13.0 | 427 | 1 YKPC | citrate (s1)-synth |
| 34 | 315.5 | 13.0 | 427 | 2 AY9722 | citrate synthase l |
| 35 | 315 | 12.9 | 437 | 2 AE3356 | citrate (s1)-synth |
| 36 | 314 | 12.9 | 424 | 2 I39506 | citrate (s1)-synth |
| 37 | 313 | 12.8 | 429 | 2 D82669 | citrate synthase X |
| 38 | 311.5 | 12.8 | 436 | 1 YKRECP | citrate (s1)-synth |
| 39 | 309.5 | 12.7 | 427 | 2 H85572 | citrate synthase l |
| 40 | 309 | 12.7 | 431 | 2 B82119 | citrate synthase v |
| 41 | 307.5 | 12.6 | 431 | 2 I40044 | citrate (s1)-synth |
| 42 | 304 | 12.5 | 429 | 2 AH2747 | citrate synthase l |
| 43 | 304 | 12.5 | 429 | 2 G97528 | citrate synthase l |
| 44 | 303.5 | 12.5 | 367 | 2 B72394 | citrate synthase l |
| 45 | 303.5 | 12.5 | 427 | 2 AF0590 | citrate synthase l |

ALIGNMENTS

RESULT 1

YKPG citrate (s1)-synthase (EC 4.1.3.7) precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 15-Oct-1982 #sequence, revision 30-Sep-1992 #text_change 05-May-2000

C:Accession: A29966; A01109; A61347

R:Evans, C.T.; Owens, D.D.; Smedley, B.; Kispal, G.; Stene, P.A.

Biochemistry 27, 4680-4686, 1988

A:Title: Isolation, nucleotide sequence, and expression of a cDNA encoding pig citre

A:Reference number: A29966; MUID:8900065; PMID:3048387

A:Accession: A29966

A:Molecule type: mRNA

A:Residues: 1-464 <EYA>

A:Cross-references: EMBL:M21197; NID:9164418; PID:AA31017.1; PID:9164419

R:Biochem, D.P.; Parmelee, D.C.; Kumar, S.; Walsh, K.A.; Titani, K.

Biochemistry 21, 2028-2036, 1982

A:Title: Complete amino acid sequence of porcine heart citrate synthase:

A:Reference number: A90457; MUID:82231993; PMID:7093227

A:Accession: A01109

A:Molecule type: protein

A:Residues: 28-464 <BLO>

R:Biochem, D.P.; Parmelee, D.C.; Kumar, S.; Wade, R.D.; Ericsson, L.H.; Neurath, H.;

Proc. Natl. Acad. Sci. U.S.A. 78, 5381-5385, 1981

A:Title: Primary structure of porcine heart citrate synthase.

A:Reference number: A61347; MUID:82060250; PMID:6795632

A:Accession: A61347

A:Molecule type: protein

A:Residues: 28-464 <BL2>

R:Remington, S.; Wiegand, G.; Huber, R.

J. Mol. Biol. 158, 111-152, 1982

A:Title: Crystallographic refinement and atomic models of two different forms of cit

A:Contents: annotation; X-ray crystallography, 2.7 and 1.7 angstroms

A:Comment: Citrate (s1)-synthase is found in nearly all cells capable of oxidative l

ycle.

C:Comment: It is synthesized in the cytoplasm but functions in the mitochondrion of

C:Comment: This molecule is a dimer of identical chains. Each dimer binds two molec

C:Superfamily: citrate (s1)-synthase

C:Keywords: carbon-carbon lyase; coenzyme A; homodimer; methylated amino acid; mitoc

F:1-27/Domains: transit peptide (mitochondrion) #status predicted <SIG>

F:28-464/Product: citrate (s1)-synthase #status experimental <MAT>

F:301,347,402/Active site: His, His, Asp #status predicted

F:395/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental

Query Match

Best Local Similarity 96.0%; Score 2339; DB 1; Length 464;

Matches 446; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

0Y 1 MALTTAAARLGTGNASCLVLAARHASASNTKDLADLIPKROARKTFRROHGKTVV 60
DB 1 MALTTAAARLGTGNASCLVLAARHASASNTKDLADLIPKROARKTFRROHGKTVV 60

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QY 61 GQITVDMVYGMGRKGLVYETSVLPDDEGTREGEFTPECOKLLPKAKGEEPLPEGLF 120
 |||||||
 DB 61 GQITVDMVYGMGRKGLVYETSVLPDDEGTREGEFTPECOKLLPKAKGEEPLPEGLF 120
 QY 121 WLLVYGHIPTEEQVWMLSEKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVATLANSBN 180
 |||||||
 DB 121 WLLVYGHIPTEEQVWMLSEKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVATLANSBN 180
 QY 181 FARAVAGISRTKYWELIYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSHNF 240
 |||||||
 DB 181 FARAVAGISRTKYWELIYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSHNF 240
 QY 241 TMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGLAGPL 300
 |||||||
 DB 241 TMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGLAGPL 300
 QY 301 HGLANQEVLMVLTQLOKEVGVDSDEKLDYIMNTLNSGRVVPYGVHAYLRKTDPRYTQ 360
 |||||||
 DB 301 HGLANQEVLMVLTQLOKEVGVDSDEKLDYIMNTLNSGRVVPYGVHAYLRKTDPRYTQ 360
 QY 361 REFALKHLPNDPMFKLVQOLYKIVPNVLLQEGKAKNPNVNDASHGVLLQYTGEMNTY 420
 |||||||
 DB 361 REFALKHLPNDPMFKLVQOLYKIVPNVLLQEGKAKNPNVNDASHGVLLQYTGEMNTY 420
 QY 421 TVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFDVSK 464
 |||||||
 DB 421 TVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFDVSK 464

RESULT 2

citrate (sl)-synthase (EC 4.1.3.7) precursor - *Caenorhabditis elegans*
 C:Species: *Caenorhabditis elegans*
 C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 05-May-2000
 C:Accession: S42370
 R:Smith, A.
 Submitted to the EMBL Data Library, March 1994
 A:Reference number: S42368
 A:Accession: S42370
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-468 <SMI>
 A:Cross-references: EMBL:Z30423; NID:G458479; PID:G458482
 C:Genetics:
 A:Introns: 69/3; 202/3; 309/3
 A:Superfamily: citrate (sl)-synthase
 C:Keywords: carbon-carbon lyase; coenzyme A; mitochondrion; oxo-acid-lyase

Query Match 69.5%; Score 1693; DB 2; Length 468;

Best Local Similarity 68.3%; Pred. No. 3,9e-120;

Matches 315; Conservative 62; Mismatches 82; Indels 2; Gaps 1;

QY 1 MALLTAARLLGTAKNA--SCLVLAARHNASSTNLKDLIDLIPKEDARKITRROHGKT 58
 |||
 DB 1 MSLSGMARILRLITKGVIPCVQVAPLSTSAEGSTLKLKIPAHNAKVSPTTEHGT 60
 QY 59 VNGQITVDMVYGMGRKGLVYETSVLPDDEGTREGEFTPECOKLLPKAKGEEPLPEG 118
 |||
 DB 59 VNGQITVDMVYGMGRKGLVYETSVLPDDEGTREGEFTPECOKLLPKAKGEEPLPEG 120
 QY 119 LFWLLVYGHIPTEEQVWMLSEKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVATLANSN 178
 |||
 DB 119 LFWLLVYGHIPTEEQVWMLSEKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVATLANSN 180
 QY 121 IWWLLCTGVDPSEQOTAAITKEMNARADLPHTVVRMLDNFPTNLHPMSQLSAAVATLANSN 180
 |||
 DB 121 IWWLLCTGVDPSEQOTAAITKEMNARADLPHTVVRMLDNFPTNLHPMSQLSAAVATLANSN 180
 QY 179 SNEFARAVAGISRTKYWELIYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSH 238
 |||
 DB 179 SNEFARAVAGISRTKYWELIYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSH 240
 QY 181 SKFAGAVARVAKKASYEAYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSH 240
 |||
 DB 181 SKFAGAVARVAKKASYEAYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSH 240
 QY 239 NFWMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGLAG 298
 |||
 DB 239 NFWMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGLAG 300
 QY 241 NFWMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGLAG 300
 |||
 DB 241 NFWMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGLAG 300
 QY 299 PLHGLANQEVLMVLTQLOKEVGVDSDEKLDYIMNTLNSGRVVPYGVHAYLRKTDPRYT 358

|||||||
 DB 301 PLHGLANQEVLMVLTQLOKEVGVDSDEKLDYIMNTLNSGRVVPYGVHAYLRKTDPRYT 360
 QY 359 COREFALKHLPNDPMFKLVQOLYKIVPNVLLQEGKAKNPNVNDASHGVLLQYTGEMNTY 418
 |||||||
 DB 361 COREFALKHLPNDPMFKLVQOLYKIVPNVLLQEGKAKNPNVNDASHGVLLQYTGEMNTY 420
 QY 419 YTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFDVSK 459
 |||||||
 DB 421 YTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFDVSK 461

RESULT 3

citrate synthase precursor, mitochondrial - fission yeast (*Schizosaccharomyces pombe*)
 C:Species: *Schizosaccharomyces pombe*
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
 C:Accession: T39028
 R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 Submitted to the EMBL Data Library, February 1996
 A:Reference number: 221750
 A:Accession: T39028
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-473 <DEV>
 A:Cross-references: EMBL:Z69731; PID:CAA93617.2; GSPDB:GNO0066; SPDB:SPAC6C3.04
 A:Experimental source: strain 972h-; cosmid 6C3
 C:Genetics:
 A:Gene: SPDB:SPAC6C3.04
 A:Map position: 1
 A:Genome: nuclear
 C:Superfamily: citrate (sl)-synthase
 C:Keywords: mitochondrion

Query Match 62.4%; Score 1519; DB 2; Length 473;

Best Local Similarity 61.3%; Pred. No. 5,6e-107;

Matches 287; Conservative 75; Mismatches 96; Indels 10; Gaps 3;

QY 6 AAARLLGTAKNACVLAARNA-----SASTNLKDLIDLIPKEDARKITRROHGKT 57
 |||
 DB 7 ASTRRLASSLSLSQASLSRQNLPLFTSSYSTSSLSKDLRLAEIKPEKQAEIKFPAEHGO 66
 QY 58 TVVQITVDMVYGMGRKGLVYETSVLPDDEGTREGEFTPECOKLLPKAKGEEPLPE 117
 |||
 DB 58 TVVQITVDMVYGMGRKGLVYETSVLPDDEGTREGEFTPECOKLLPKAKGEEPLPE 126
 QY 67 DIVGEVTTINOMYGGARGVSLIMBSGVLPDDEGTREGEFTPECOKLLPKAKGEEPLPE 126
 |||
 DB 67 DIVGEVTTINOMYGGARGVSLIMBSGVLPDDEGTREGEFTPECOKLLPKAKGEEPLPE 126
 QY 118 GLFWLLVYGHIPTEEQVWMLSEKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVATLANS 177
 |||
 DB 127 SLFWLLVYGHIPTEEQVWMLSEKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVATLANS 186
 QY 178 ESNEFARAVAGISRTKYWELIYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSH 237
 |||
 DB 187 DSNEFARAVAGISRTKYWELIYEDSMDLAKLPCVAARIYRNLVREGSGIGADISNDWSH 245
 QY 238 HNFNTMLGTYDHOFTELRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGL 296
 |||
 DB 246 YNFANVLAGFANNEFEVLMKRLTYITSHDHEGCVNSAHTSHVGSALSDPLSPFAAMNGL 305
 QY 297 AGPLHGLANQEVLMVLTQLOKEVGVDSDEKLDYIMNTLNSGRVVPYGVHAYLRKTDPR 356
 |||
 DB 306 AGPLHGLANQEVLMVLTQLOKEVGVDSDEKLDYIMNTLNSGRVVPYGVHAYLRKTDPR 365
 QY 357 YTCOREFALKHLPNDPMFKLVQOLYKIVPNVLLQEGKAKNPNVNDASHGVLLQYTGEMNTY 416
 |||
 DB 366 YTCOREFALKHLPNDPMFKLVQOLYKIVPNVLLQEGKAKNPNVNDASHGVLLQYTGEMNTY 425
 QY 417 MNYTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFDVSK 464
 |||
 DB 426 QSEYTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFDVSK 473

RESULT 4

T49379

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OM protein - protein search, using sw model

Run on: September 5, 2003, 20:02:07 ; Search time 43 Seconds
(without alignments)
1720.153 Million cell updates/sec

Title: US-09-996-223-1

Perfect score: 2436

Sequence: 1 MALTTAAARLGTGNASCLV.....ERPKSMSTEGLMKRFVDSKSG 466

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

A.Geneseq_19Jun03:.*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
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8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
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14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2436 | 100.0 | 466 | 22 | AAAG3432 |
| 2 | 2436 | 100.0 | 466 | 23 | ABG32120 |
| 3 | 2436 | 100.0 | 466 | 23 | ABB05627 |
| 4 | 2339 | 96.0 | 464 | 23 | ABG32121 |
| 5 | 1737.5 | 71.3 | 464 | 22 | ABB60227 |
| 6 | 1498.5 | 61.5 | 442 | 21 | AAAG10538 |
| 7 | 1498.5 | 61.5 | 442 | 21 | AAAG32322 |
| 8 | 1498.5 | 61.5 | 442 | 21 | AAAG40501 |
| 9 | 1498.5 | 61.5 | 473 | 21 | AAAG10537 |

| | | | | | |
|----|--------|------|-----|----|-----------|
| 10 | 1498.5 | 61.5 | 473 | 21 | AAAG40500 |
| 11 | 1498.5 | 61.5 | 474 | 21 | AAAG32321 |
| 12 | 1493 | 61.3 | 466 | 21 | AAAG50501 |
| 13 | 1480.5 | 60.8 | 437 | 16 | AAAB82839 |
| 14 | 1439 | 59.1 | 469 | 16 | AAAB82840 |
| 15 | 1425 | 58.5 | 460 | 23 | ABG93057 |
| 16 | 1402.5 | 57.6 | 400 | 21 | AAAG10539 |
| 17 | 1402.5 | 57.6 | 400 | 21 | AAAG32323 |
| 18 | 1402.5 | 57.6 | 400 | 21 | AAAG40502 |
| 19 | 1385.5 | 56.9 | 397 | 23 | ABG93310 |
| 20 | 1349 | 55.4 | 471 | 16 | AAAB82838 |
| 21 | 1349 | 55.4 | 471 | 16 | AAAB83833 |
| 22 | 1157 | 47.5 | 407 | 22 | ABAB69749 |
| 23 | 571 | 23.4 | 116 | 22 | ABAB44416 |
| 24 | 571 | 23.4 | 116 | 22 | ABAB72264 |
| 25 | 571 | 23.4 | 116 | 22 | AAAB78158 |
| 26 | 571 | 23.4 | 116 | 22 | AAAB22030 |
| 27 | 571 | 23.4 | 116 | 22 | AAAB38402 |
| 28 | 571 | 23.4 | 116 | 23 | ABG47171 |
| 29 | 522 | 21.4 | 104 | 21 | AAAG00253 |
| 30 | 362.5 | 14.9 | 430 | 22 | AAAB83188 |
| 31 | 356 | 14.6 | 431 | 22 | AAAB79515 |
| 32 | 356 | 14.6 | 437 | 22 | AAAG93187 |
| 33 | 353 | 14.5 | 436 | 12 | AAAR14357 |
| 34 | 353 | 14.5 | 437 | 22 | AAAB83189 |
| 35 | 345.5 | 14.2 | 437 | 24 | ABP79498 |
| 36 | 339.5 | 13.9 | 514 | 23 | ABAB92726 |
| 37 | 338 | 13.9 | 509 | 23 | ABAB92085 |
| 38 | 329 | 13.5 | 132 | 21 | AAAG26766 |
| 39 | 325 | 13.3 | 101 | 21 | AAAG26768 |
| 40 | 325 | 13.3 | 116 | 21 | AAAG26767 |
| 41 | 320 | 13.1 | 134 | 22 | AAAM00061 |
| 42 | 320 | 13.1 | 441 | 23 | ABAB53981 |
| 43 | 315.5 | 13.0 | 427 | 21 | AAAB15967 |
| 44 | 315.5 | 13.0 | 427 | 22 | AAAB29342 |
| 45 | 310.5 | 12.7 | 489 | 22 | AAU67471 |

ALIGNMENTS

| | | |
|----------|---|----------------------------|
| RESULT 1 | AAAG3432 | standard; Protein: 466 AA. |
| ID | AAAG3432 | |
| AC | AAAG3432 | |
| DT | 06-NOV-2001 | (first entry) |
| DE | Human polypeptide, SEO ID NO: 3064. | |
| DE | Human; full length cDNA; cDNA synthesis; oligo-capping. | |
| OS | Homo sapiens. | |
| PN | EP1130094-A2. | |
| XX | 05-SEP-2001. | |
| PF | 07-JUL-2000; 2000EP-0114089. | |
| PR | 08-JUL-1999; 99JP-0194486. | |
| PR | 11-JAN-2000; 2000JP-0118774. | |
| PR | 02-MAY-2000; 2000JP-0183765. | |
| XX | (HELI-) HELIX RES INST. | |
| PA | Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y; | |
| PI | Wakematsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H; | |
| XX | WPI, 2001-524255/58. | |
| DR | N-PSDB; AAK94353. | |

Arabidopsis thalia
Arabidopsis thalia
Candida albicans p
Sugar beet citrate
Tobacco citrate sy
S. cerevisiae BAX-
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
C. albicans BAX-as
Potato citrate syn
Potato citrate syn
Drosophila melanog
Peptide #11922 enc
Protein #9263 enco
Human bone marrow
Peptide #8464 enco
Peptide #12439 enc
Human secreted pro
Corynebacterium th
Corynebacterium gl
C. glutamicum prote
Citrate synthase e
Brevibacterium lac
N. gonorrhoeae ami
Herbicidally activ
Herbicidally activ
Zea mays protein f
Zea mays protein f
Zea mays protein f
Citrate synthetase
Lactococcus lactis
E. coli proliferat
Novel mat regulate
Protonibacterium

PT 830 Primers useful for synthesizing full length cDNA clones and their
 PT use in genetic manipulation -
 XX
 XX
 PS Claim 8; SEQ ID NO 3064; 1380bp + sequence listing; English.
 XX
 CC The invention relates to primers for synthesizing full length cDNA
 CC clones. 830 cDNA molecules encoding a human protein have been
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
 CC molecules have been determined. Primers for synthesizing the full length
 CC cDNA are useful for clarifying the function of the protein encoded by
 CC the cDNA. The full length clones were obtained by construction of full
 CC length enriched cDNA libraries that were synthesised by the oligo-capping
 CC method. The primers enable the production of the full length cDNA easily
 CC without any special methods. The present sequence is a polypeptide
 CC encoded by a full length human cDNA of the invention.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in CD-ROM format directly from EPO.
 CC
 XX
 SO Sequence 466 AA;
 Query Match 100.0%; Score 2436; DB 22; Length 466;
 Best Local Similarity 100.0%; Pred. No. 2,7e-219;
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALLTAARLGLTRKNSCLVLARHNASSTNLKDLADLIPKQARIKTFROHKTIV 60
 DB 1 MALLTAARLGLTRKNSCLVLARHNASSTNLKDLADLIPKQARIKTFROHKTIV 60
 QY 61 GQITVDMYMGKMGKGLVETSVLDPEDEGIRFGSGFISPCOKLLPRAKGGEPLPGLE 120
 DB 61 GQITVDMYMGKMGKGLVETSVLDPEDEGIRFGSGFISPCOKLLPRAKGGEPLPGLE 120
 QY 121 WLLVTGHIPTREOVSWLSKEMAKRALPSHVVTMLDNFPNLHPMSQLSAAYTALNSEN 180
 DB 121 WLLVTGHIPTREOVSWLSKEMAKRALPSHVVTMLDNFPNLHPMSQLSAAYTALNSEN 180
 QY 181 FARAYNGISRTKYWEIYDSDMLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
 DB 181 FARAYNGISRTKYWEIYDSDMLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
 QY 241 TNNLGYTDHOFTELTRLYTIHSDHEGANSATSHSLVGSALSDPYSPFAAMNGLGPL 300
 DB 241 TNNLGYTDHOFTELTRLYTIHSDHEGANSATSHSLVGSALSDPYSPFAAMNGLGPL 300
 QY 301 HGLANDEVLMVLTQLOKEVSKDVSDKRLROYIMNTLNSGAVVPDYGHAVALRKTDPRYTCQ 360
 DB 301 HGLANDEVLMVLTQLOKEVSKDVSDKRLROYIMNTLNSGAVVPDYGHAVALRKTDPRYTCQ 360
 QY 361 REFALKRLPNDPMEKLVLAOLYKIVPNVLLFOGKAKNPWPVDAHSGVLLQYGTETENNY 420
 DB 361 REFALKRLPNDPMEKLVLAOLYKIVPNVLLFOGKAKNPWPVDAHSGVLLQYGTETENNY 420
 QY 421 TVLFQVSRAFGVLAQLWISRALGFPLEPRKSMSTEGIMKRVDSKSG 466
 DB 421 TVLFQVSRAFGVLAQLWISRALGFPLEPRKSMSTEGIMKRVDSKSG 466
 RESULT 2
 ABG32120 standard; Protein; 466 AA.
 ID ABG32120;
 AC ABG32120;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Human citrate synthase homologue (HUCS).
 XX
 KW Human; citrate synthase homologue; HUCS; cancer; inflammatory disorder;
 KW acquired immunodeficiency syndrome; AIDS; Addison's disease; allergy;
 KW anaemia; asthma; atherosclerosis; bronchitis; Crohn's disease;
 KW ulcerative colitis; atopic dermatitis; diabetes mellitus; emphysema;
 KW glomerulonephritis; gout; Grave's disease; lupus erythematosus;
 KW multiple sclerosis; myasthenia gravis; myocardial inflammation;

KW pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;
 KW rheumatoid arthritis; scleroderma; Sjogren's syndrome; haemodialysis;
 KW autoimmune thyroiditis; extracorporeal infection; circulation;
 KW viral infection; bacterial infection; fungal infection; arrhythmia;
 KW parasitic infection; protozoal infection; helminthic infection; trauma;
 KW sympathetic nervous system disorder; angina; anaphylactic shock;
 KW asthma; cardiovascular shock; Cushing's syndrome; hypertension;
 KW hypoglycaemia; myocardial infarction; migraine; pheochromocytoma;
 KW transgenic animal.
 XX
 OS Homo sapiens.
 XX
 PN US200209195-A1.
 XX
 PD 25-JUL-2002.
 XX
 PF 27-NOV-2001; 2001US-0996223.
 XX
 PR 13-NOV-1997; 97US-0970134.
 XX
 PA (INCY-) INCYTE PHARM INC.
 XX
 PI Hillman JL, Lal P, Corley NC, Shah P;
 DR WPI, 2002-666037/71.
 DR N-PSDB; ABK90783.
 XX
 PT New human citrate synthase homologue polypeptide for diagnosing and
 PT treating cancer, inflammatory disorders and disorders of the
 PT sympathetic nervous system e.g. angina, and anaphylactic shock -
 XX
 PS Claim 1; Fig 1A-F; 35pp; English.
 XX
 CC The invention describes an isolated human citrate synthase homologue
 CC (HUCS) polypeptide (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist useful for treating a disease
 CC or condition associated with altered expression of functional HUCS in a
 CC patient. (II), the encoding nucleic acid (II) and modulators of (I) are
 CC useful for diagnosis, treatment and prevention of cancer, inflammatory
 CC disorders such as acquired immunodeficiency syndrome (AIDS), Addison's
 CC disease, allergies, anaemia, asthma, atherosclerosis, bronchitis, Crohn's
 CC disease, ulcerative colitis, atopic dermatitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, Grave's disease, lupus
 CC erythematosus, multiple sclerosis, myasthenia gravis, myocardial or
 CC pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis,
 CC rheumatoid arthritis, scleroderma, Sjogren's syndrome, and autoimmune
 CC thyroiditis, complications of cancer, haemodialysis and extracorporeal
 CC circulation, viral, bacterial, fungal, parasitic, protozoal and
 CC helminthic infections and trauma, and disorders of the sympathetic
 CC nervous system including angina, anaphylactic shock, arrhythmias, asthma,
 CC cardiovascular shock, Cushing's syndrome, hypertension, hypoglycaemia,
 CC myocardial infarction, migraine and pheochromocytoma. (II) is useful for
 CC creating knockin humanised animals or transgenic animals to model human
 CC disease and to detect and quantify gene expression in biopsied tissues in
 CC which expression of HUCS is correlated with disease. (II) is also useful
 CC for generating hybridisation probes useful in mapping the naturally
 CC occurring genomic sequence and oligonucleotide primers derived from
 CC (II) are useful to detect single nucleotide polymorphisms. HUCS,
 CC fragments of it and antibodies specific for HUCS are useful as elements
 CC on a microarray which is useful to monitor or measure protein-protein
 CC interactions, drug-target interactions and gene expression profiles. This
 CC is the amino acid sequence of the human citrate synthase homologue
 CC (HUCS).
 CC
 XX
 SO Sequence 466 AA;
 Query Match 100.0%; Score 2436; DB 23; Length 466;
 Best Local Similarity 100.0%; Pred. No. 2,7e-219;
 Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALLTAARLGLTRKNSCLVLARHNASSTNLKDLADLIPKQARIKTFROHKTIV 60
 DB 1 MALLTAARLGLTRKNSCLVLARHNASSTNLKDLADLIPKQARIKTFROHKTIV 60

QY 61 GOITVDMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKAKGEEPLPEGLF 120
 DB 61 GOITVDMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKAKGEEPLPEGLF 120
 QY 121 WLVYGHIPTEBOVSWSLSEKAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSES 180
 DB 121 WLVYGHIPTEBOVSWSLSEKAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSES 180
 QY 181 FARAVAGISRTKYWELIYEDSMDLIAKLPVAAKTYRNLREGSGIGADISNLDMSHNF 240
 DB 181 FARAVAGISRTKYWELIYEDSMDLIAKLPVAAKTYRNLREGSGIGADISNLDMSHNF 240
 QY 241 TNLGTYDHOFTETRLTYLTTHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
 DB 241 TNLGTYDHOFTETRLTYLTTHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
 QY 301 HGLANQEVLVMTQLQKEVGKDVSDKLRDYIMNTLNSGRVVPYGYHAVALRKTDPRYTQ 360
 DB 301 HGLANQEVLVMTQLQKEVGKDVSDKLRDYIMNTLNSGRVVPYGYHAVALRKTDPRYTQ 360
 QY 361 REFALKHLPNPMFKLVNQLYKIVPNVLLBEGKAKNPMPNDASHGVLLQYTGTEMY 420
 DB 361 REFALKHLPNPMFKLVNQLYKIVPNVLLBEGKAKNPMPNDASHGVLLQYTGTEMY 420
 QY 421 TVLFQVSRAALGVLAQLIWSRALGFLPRLPKSMSTEGLMKPFVDSKSG 466
 DB 421 TVLFQVSRAALGVLAQLIWSRALGFLPRLPKSMSTEGLMKPFVDSKSG 466

RESULT 3

ABB05627 ID ABB05627 standard; Protein; 466 AA.

AC ABB05627;

DT 25-APR-2002 (first entry)

DE Human citrate synthase homologue (HUCS) protein SEQ ID NO:1.

KM Human: citrate synthase homologue; HUCS; enzyme: cytosolic; neotropic;

KM antiinflammatory; neuroprotective; citrate synthase; gene therapy;

KM cancer; inflammatory disorder; sympathetic nervous system disorder.

OS Homo sapiens.

PN US6323328-B1.

PD 27-NOV-2001.

PF 13-NOV-1997; 97US-0970134.

PR 13-NOV-1997; 97US-0970134.

PA (INCY-) INCYTE GENOMICS INC.

PI Hillman JL, Lal P, Corley NC, Shah P;

DR WPI: 2002-163049/21.

DR N-PSDB: ABB93492.

PT New polynucleotide encoding a human citrate synthase homologue for

PT preventing or treating cancer, inflammatory disorders and disorders of

PT the sympathetic nervous system

PS Claim 1; Fig 1A-F; 31pp; English.

CC The present sequence represents a human citrate synthase homologue

CC (HUCS) protein (I), (II), and the polynucleotide (II) encoding (I), have

CC cytosolic, antiinflammatory, neuroprotective and neotropic activities,

CC and can be used in gene therapy. (II) can be used to produce a HUCS

CC polypeptide. (I) and (II) can be used to prevent or treat disorders

CC associated with HUCS expression, particularly cancer, an inflammatory

CC: disorder or a disorder of the sympathetic nervous system.

XX sequence 466 AA;

SO Query Match 100.0%; Score 2436; DB 23; Length 466;

Best Local Similarity 100.0%; Pred. No. 2,7e-219;

Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALTTAARILGKTNASCLVLAARHASSTNLDLIADLIPKEQARIKTFROOGKTVV 60
 DB 1 MALTTAARILGKTNASCLVLAARHASSTNLDLIADLIPKEQARIKTFROOGKTVV 60
 QY 61 GOITVDMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKAKGEEPLPEGLF 120
 DB 61 GOITVDMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKAKGEEPLPEGLF 120
 QY 121 WLVYGHIPTEBOVSWSLSEKAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSES 180
 DB 121 WLVYGHIPTEBOVSWSLSEKAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSES 180
 QY 181 FARAVAGISRTKYWELIYEDSMDLIAKLPVAAKTYRNLREGSGIGADISNLDMSHNF 240
 DB 181 FARAVAGISRTKYWELIYEDSMDLIAKLPVAAKTYRNLREGSGIGADISNLDMSHNF 240
 QY 241 TNLGTYDHOFTETRLTYLTTHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
 DB 241 TNLGTYDHOFTETRLTYLTTHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
 QY 301 HGLANQEVLVMTQLQKEVGKDVSDKLRDYIMNTLNSGRVVPYGYHAVALRKTDPRYTQ 360
 DB 301 HGLANQEVLVMTQLQKEVGKDVSDKLRDYIMNTLNSGRVVPYGYHAVALRKTDPRYTQ 360
 QY 361 REFALKHLPNPMFKLVNQLYKIVPNVLLBEGKAKNPMPNDASHGVLLQYTGTEMY 420
 DB 361 REFALKHLPNPMFKLVNQLYKIVPNVLLBEGKAKNPMPNDASHGVLLQYTGTEMY 420
 QY 421 TVLFQVSRAALGVLAQLIWSRALGFLPRLPKSMSTEGLMKPFVDSKSG 466
 DB 421 TVLFQVSRAALGVLAQLIWSRALGFLPRLPKSMSTEGLMKPFVDSKSG 466

RESULT 4

ABG32121 ID ABG32121 standard; Protein; 464 AA.

AC ABG32121;

DT 15-NOV-2002 (first entry)

DE Pig citrate synthase homologue (HUCS).

KM Pig: citrate synthase homologue; HUCS; cancer; inflammatory disorder;

KM acquired immunodeficiency syndrome; AIDS; Addison's disease; allergy;

KM anaemia; asthma; atherosclerosis; bronchitis; Crohn's disease;

KM ulcerative colitis; atopic dermatitis; diabetes mellitus; emphysema;

KM glomerulonephritis; gout; Grave's disease; lupus erythematosus;

KM multiple sclerosis; myasthenia gravis; myocardial inflammation;

KM pericardial inflammation; osteoarthritis; osteoporosis; pancreatitis;

KM rheumatoid arthritis; scleroderma; Sjogren's syndrome; haemodialysis;

KM autoimmune thyroiditis; extracorporeal infection; circulation;

KM viral infection; bacterial infection; fungal infection; arhythmia;

KM parasitic infection; protozoal infection; helminthic infection; trauma;

KM sympathetic nervous system disorder; angina; anaphylactic shock;

KM asthma; cardiovascular shock; Cushing's syndrome; hypertension;

KM hypoglycaemia; myocardial infarction; migraine; pheochromocytoma;

KM transgenic animal.

OS Sus scrofa.

PN US2002099195-A1.

PD 25-JUL-2002.

PF 27-NOV-2001: 200JUS-0996223.
 XX
 PR 13-NOV-1997: 97US-0970134.
 PA (INCY-) INCYTE PHARM INC.
 PI Hillman JL, Lal P, Corley NC, Shah P;
 XX WPI; 2002-666037/1.
 DR
 XX
 PT New human citrate synthase homolog polypeptide for diagnosing and
 PT treating cancer, inflammatory disorders and disorders of the
 PT sympathetic nervous system e.g. angina, and anaphylactic shock -
 XX
 PS Disclosure; Fig 2A-B; 35pp; English.
 XX
 CC The invention describes an isolated human citrate synthase homologue
 CC (HUCS) polypeptide (I). (I) is useful for screening a compound for
 CC effectiveness as an agonist or antagonist useful for treating a disease
 CC or condition associated with altered expression of functional HUCS in a
 CC patient. (II), the encoding nucleic acid (II) and modulators of (I) are
 CC useful for diagnosis, treatment and prevention of cancer, inflammatory
 CC diseases such as acquired immunodeficiency syndrome (AIDS), Addison's
 CC disease, allergies, anaemia, asthma, atherosclerosis, bronchitis, Crohn's
 CC disease, ulcerative colitis, atopic dermatitis, diabetes mellitus,
 CC emphysema, glomerulonephritis, gout, grave's disease, lupus
 CC erythematosus, multiple sclerosis, myasthenia gravis, myocardial or
 CC pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis,
 CC rheumatoid arthritis, scleroderma, Sjogren's syndrome, and autoimmune
 CC thyroiditis, complications of cancer, haemodialysis and extracorporeal
 CC circulation, viral, bacterial, fungal, parasitic, protozoal and
 CC helminthic infections and trauma, and disorders of the sympathetic
 CC nervous system including angina, anaphylactic shock, arrhythmias, asthma,
 CC cardiovascular shock, Cushing's syndrome, hypertension, hypoglycaemia,
 CC myocardial infarction, migraine and pheochromocytoma. (II) is useful for
 CC creating knockin humanised animals or transgenic animals to model human
 CC disease and to detect and quantify gene expression in biopsied tissues in
 CC which expression of HUCS is correlated with disease. (II) is also useful
 CC for generating hybridisation probes useful in mapping the naturally
 CC occurring genomic sequence and oligonucleotide polymorphisms. HUCS,
 CC (II) are useful to detect single nucleotide polymorphisms. HUCS,
 CC fragments of it and antibodies specific for HUCS are useful as elements
 CC on a microarray which is useful to monitor or measure protein-protein
 CC interactions, drug-target interactions and gene expression profiles. This
 CC is the amino acid sequence of the pig citrate synthase homologue (HUCS).
 CC
 XX
 SQ Sequence 464 AA:
 Query Match 96.0%; Score 2339; DB 23; Length 464;
 Best Local Similarity 96.1%; Pred. No. 3,3e-210;
 Matches 446; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

DB 301 HGLANDEVLMTLQLOKEVGKDVSDKRLRYINWTLNSGRVVPYGHAVLRKTDPRYTCQ 360
 QY 361 REFALKHLPPNDPMFKLVAQLYKIVPNVLEBOGRKAKNPVNDASHGVLLOYYGMTENNY 420
 DB 361 REFALKHLPPNDPMFKLVAQLYKIVPNVLEBOGRKAKNPVNDASHGVLLOYYGMTENNY 420
 QY 421 TVLFGVSRALGVLAQLIWSRALGFPLEPRKSMSTEGILMKFVDSK 464
 DB 421 TVLFGVSRALGVLAQLIWSRALGFPLEPRKSMSTEGILMKFVDSK 464
 RESULT 5
 ID ABB60227 standard; Protein: 464 AA.
 XX
 AC ABB60227;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Drosophila melanogaster polypeptide SEQ ID NO 7473.
 XX
 KW Drosophila; developmental biology; cell signalling; insecticide;
 KW pharmaceutical.
 XX
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 PD 27-SEP-2001.
 XX
 PF 23-MAR-2001; 2001WO-US09221.
 XX
 PR 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 XX
 PI Venter JC, Adams M, Li PWD, Myers EW;
 XX
 DR WPI; 2001-656860/75.
 DR N-PSDB; ABL04330.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 7473; 21pp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABB57737-ABB72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX
 SQ Sequence 464 AA:
 Query Match 71.3%; Score 1737.5; DB 22; Length 464;
 Best Local Similarity 70.5%; Pred. No. 7.7e-154;
 Matches 328; Conservative 50; Mismatches 80; Indels 7; Gaps 2;

Db 58 ATKMGETTIDMWGNGRIKALVETSVLDADEGIRFRLGLSIPBECOKVLPAAADGTEPLP 117
QY 117 EGLFLLVTHGHIPTERQVSMLSKEMAKRALPESHVVTMLDNPTNLHPMSQLSAAYTALN 176
Db 118 EGLFLLVTHGHIPTERQVSMLSKEMAKRALPESHVVTMLDNPTNLHPMSQLSAAYTALN 177
QY 177 SSNFAVAYAOGISRTKWEYLIEDSMDLIAKLPCVAARIYRLYREGSGIGAIDENLDM 236
Db 178 HDSKFAKAYSDGVHKSKEYEYEDSMDLIAKLPCVAARIYRLYREGSGIGAIDENLDM 237
QY 237 SHNFTMLGYTDHOFELTRLYTTHSDHGGVNSAHTSLVGSALSADPYLSAAMNGL 296
Db 238 SANFVAMLGVDNAPFELMRLYTTHSDHGGVNSAHTSLVGSALSADPYLSAAMNGL 297
QY 297 AGPLHGLANQEVLYMLTQLOKEVGKDVSEKLELDYIMNTLNSGRVYPGYGHAVLRKTDPR 356
Db 298 AGPLHGLANQEVLYMLTQLOKEVGKDVSEKLELDYIMNTLNSGRVYPGYGHAVLRKTDPR 357
QY 357 YTCQREFALKHLPNDEMFRLVAQLYKIVPNVLLDGGKAKNPMPNDASHGVLLQYYGME 416
Db 358 YTCQREFALKHLPEDETFQLVSKIKYKVPPILETGTGKVKMPMPNDASHGVLLQYYGME 417
QY 417 MNYTYLFGVSRLQVLAQLINSRALGFPLERPKSMSTEGLMKFV 461
Db 418 MNYTYLFGVSRLQVLAQLINSRALGFPLERPKSMSTEGLMKFV 462

RESULT 6

AAG10538 standard; Protein; 442 AA.

AC AAG10538;

DT 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 8901.

KM Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KM termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134421.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 23-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.

PR 23-MAR-1999; 990S-0125788.
PR 25-MAR-1999; 990S-0126264.
PR 29-MAR-1999; 990S-0126785.
PR 01-APR-1999; 990S-0127462.
PR 06-APR-1999; 990S-0128234.
PR 08-APR-1999; 990S-0128714.
PR 16-APR-1999; 990S-0128845.
PR 19-APR-1999; 990S-0130077.
PR 21-APR-1999; 990S-0130449.
PR 23-APR-1999; 990S-0130510.
PR 23-APR-1999; 990S-0130891.
PR 28-APR-1999; 990S-0131449.
PR 30-APR-1999; 990S-0132048.
PR 30-APR-1999; 990S-0132407.
PR 04-MAY-1999; 990S-0132484.
PR 05-MAY-1999; 990S-0132485.
PR 06-MAY-1999; 990S-0132486.
PR 06-MAY-1999; 990S-0132487.
PR 07-MAY-1999; 990S-0132863.
PR 11-MAY-1999; 990S-0134256.
PR 14-MAY-1999; 990S-0134218.
PR 14-MAY-1999; 990S-0134219.
PR 14-MAY-1999; 990S-0134221.
PR 14-MAY-1999; 990S-0134370.
PR 18-MAY-1999; 990S-0134768.
PR 19-MAY-1999; 990S-0135124.
PR 20-MAY-1999; 990S-0135124.
PR 21-MAY-1999; 990S-0135353.
PR 24-MAY-1999; 990S-0135629.
PR 25-MAY-1999; 990S-0136021.
PR 27-MAY-1999; 990S-0136392.
PR 28-MAY-1999; 990S-0136782.
PR 01-JUN-1999; 990S-0137222.
PR 03-JUN-1999; 990S-0137528.
PR 04-JUN-1999; 990S-0137502.
PR 07-JUN-1999; 990S-0137724.
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PR 29-OCT-1999: 99US-0162142.

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Best Local Similarity 62.6%; Pred. No. 1,8e-131; Matches 270; Conservative 77; Mismatches 83; Indels 1; Gaps 1;

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DB 3 SSTDDLKSQLQLLIREQODRLKKLKSEHKVQLGNTITVDMYGGKMGKGLYETSVLD 62
QY 87 PDEGIRFPGFSIPECCKLLPKAKGEEPLPEGLFWLLVYGHIPTEBOVSWLSKEMAKRA 146
DB 63 PERGIRFPGFSIPECCKVLPYTAQSGAEPLEGLFWLLVYGHIPTEBOVSWLSKEMAKRA 122
QY 147 LPSHYVTMDNPTNHPMSQLSAAYTALNSENFPARAQGISRKTYMELTYEDSMDLI 206
DB 123 VPQYVNAIDALPSTAHPMITQFASGYVALQVQSEFQKAYENGTHKSKFMEPTYEDCINI 182
QY 207 AKLPCYAAKTYRNLTYREGSGIGAIDSNLDMSHNFTWMLGYTDHOFELFRLYLTISHDHE 266
DB 183 ARPYVVAAYVRRMYKNGDSIPS-DKSLDYGANFSHMLGFDDDEKVELMRLYITISHDHE 241
QY 267 GCNVAHSHLVGALSDFYLSFAAMNGLAGPLHGLANQEVLTWLTLQKEVGDVSD 326
DB 242 GCNVAHSHLVGALSDFYLSFAAMNGLAGPLHGLANQEVLTWLTLQKEVGDVSD 301
QY 327 KLRDYIWNLTNSGRVPGYGHAVLRTKTDRTYTCQRFALKHLENDPEFKYVAOLYKIVPN 366
DB 302 QLKEVYKTLNSGKVPYGHVLRMTDPRYTCQRFALKHLENDPEFKYVAOLYKIVPN 361
QY 387 VLLEGGKAKPMNVVAHSGVLLQYGMTEEMNYTYTLFGVSRALYLAOLIWSRALGEP 446
DB 362 VLTELCKVKNPMNVVAHSGVLLNHYGLTEARYTYLVFGVSRSLGICSQLIMDRALGLAL 421
QY 447 ERPKSMSTEG 457
DB 422 ERPKSVTMDWL 432

RESULT 8
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ID AAG40501 standard; protein; 442 AA.
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AC AAG40501:
XX 18-OCT-2000 (first entry)
DT Arabidopsis thaliana protein fragment SEQ ID NO: 50261.
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DE
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
DS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
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Query Match      61.5%; Score 1498.5; DB 21; Length 473;
Best Local Similarity 62.6%; Pred. No. 2e-131;
Matches 270; Conservative 77; Mismatches 89; Indels 1; Gaps 1;

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DB 34 SSTDLKLSQLELPEQODRLKLSSEHGKVGQVLNITVDVIGMGRMGKLTMTSTILD 93
OY 87 PDEGIRFREGFSIPRECOKLLPKAKGGEPLPGILFVLVYTGHPPEQVSWLSKEWAKRAA 146
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 94 PEEGIRFREGLSIPRECOKLPTAOSGAEPPLPGLMLLTGTGVPSEKVEALSKDLANRAA 153
OY 147 LPSHVYTLMDNFPPTLHPMSOLSAAVTALNESENFARAAGISRTKWTLYEDSDMLI 206
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DB 154 VPDYVYNAIDALPSTAHMPTOPASGVMALOYOSEPOKAYENGIRKSKMEPTIEDCLNI 213
OY 207 AKLPCVAAKIYRNLYREGSGGIGAIIDSNLDSHNFMTNLGYTDHOFTELRLYTIHSDHE 266
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DB 214 ARVPVVAAYVYRRMYKNDGSDIPS-DKSIDYGANFSHMLGFDEKVKELMRLYTIHSDHE 272
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DB 273 GGNVSAHSHLVGSLSDPYLSFAAALNGLAGPLHGLANOVLYVMTQLOKEVGKDVSD 332
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OY 387 VLEEGKAKNPMPVNDASHGVLLQYGTENMYTVLFGVSRAVLQALWISRALGFPL 446
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RESULT 10
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AC AAG40500;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50260.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147202.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.

GenCore version 5.1.6
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Run on: September 5, 2003, 20:10:52 : Search time 61 Seconds
(without alignments)
1048.910 Million cell updates/sec

Title: US-09-996-223-1

Perfect score: 2436
Sequence: 1 MALTYAARLLGTAKNSCLV.....ERPKSKTEGLKFKYDSKSG 466

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513375 seqs, 137303645 residues

Total number of hits satisfying chosen parameters: 513375

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications_AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 2239 | 96.0 | 464 | US-09-996-223-3 | Sequence 3, Appl1 |
| 3 | 571 | 23.4 | 116 | US-09-864-761-42562 | Sequence 42562, A |
| 4 | 356 | 14.6 | 437 | US-09-738-626-6941 | Sequence 6941, A |
| 5 | 343.5 | 14.1 | 429 | US-10-156-761-12864 | Sequence 12864, A |
| 6 | 325 | 13.3 | 1232 | US-10-017-161-2396 | Sequence 2396, Ap |
| 7 | 320 | 13.1 | 134 | US-09-734-568-80 | Sequence 80, Appl |
| 8 | 315.5 | 13.0 | 427 | US-09-912-020-324 | Sequence 324, Appl |
| 9 | 274 | 11.2 | 426 | US-09-815-242-11282 | Sequence 11282, A |
| 10 | 257.5 | 10.6 | 367 | US-09-815-242-5427 | Sequence 5427, Ap |
| 11 | 257.5 | 10.6 | 373 | US-09-815-242-12921 | Sequence 12921, A |
| 12 | 257.5 | 10.6 | 373 | US-09-815-242-12906 | Sequence 12906, A |
| 13 | 256.5 | 10.5 | 383 | US-09-738-626-4233 | Sequence 4233, Ap |
| 14 | 240.5 | 9.9 | 388 | US-10-156-761-9964 | Sequence 9964, Ap |
| 15 | 237.5 | 9.7 | 394 | US-09-738-626-4273 | Sequence 4273, Ap |

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| 16 | 234.5 | 9.6 | 375 | 9 | US-09-815-242-11803 | Sequence 11803, A |
| 17 | 227.5 | 9.3 | 389 | 9 | US-09-815-242-10058 | Sequence 10058, A |
| 18 | 222.5 | 9.1 | 389 | 9 | US-09-815-242-13894 | Sequence 13894, A |
| 19 | 183.5 | 7.5 | 366 | 15 | US-10-156-761-11393 | Sequence 11393, A |
| 20 | 138 | 5.7 | 418 | 15 | US-10-156-761-9965 | Sequence 9965, Ap |
| 21 | 125.5 | 5.2 | 608 | 10 | US-09-344-882-12 | Sequence 12, Appl |
| 22 | 125.5 | 5.2 | 608 | 15 | US-10-293-865-12 | Sequence 12, Appl |
| 23 | 114.5 | 4.7 | 272 | 10 | US-09-344-882-10 | Sequence 10, Appl |
| 24 | 114.5 | 4.7 | 272 | 15 | US-10-293-865-10 | Sequence 10, Appl |
| 25 | 100 | 4.1 | 363 | 10 | US-09-925-300-1530 | Sequence 1530, Ap |
| 26 | 94.5 | 3.9 | 2092 | 15 | US-10-128-714-3061 | Sequence 3061, Ap |
| 27 | 94.5 | 3.9 | 2092 | 15 | US-10-128-714-8061 | Sequence 8061, Ap |
| 28 | 93 | 3.8 | 882 | 15 | US-10-156-761-15031 | Sequence 15031, A |
| 29 | 93 | 3.8 | 904 | 15 | US-10-156-761-8762 | Sequence 8762, Ap |
| 30 | 92.5 | 3.8 | 822 | 10 | US-09-981-9008-9 | Sequence 9, Appl |
| 31 | 91 | 3.7 | 297 | 9 | US-09-815-242-5206 | Sequence 5206, Ap |
| 32 | 91 | 3.7 | 601 | 15 | US-10-156-761-12207 | Sequence 12207, A |
| 33 | 90.5 | 3.7 | 828 | 15 | US-10-101-464A-934 | Sequence 934, App |
| 34 | 90.5 | 3.7 | 1039 | 12 | US-10-021-660-80 | Sequence 80, Appl |
| 35 | 90 | 3.7 | 1168 | 10 | US-09-919-603-2 | Sequence 2, Appl1 |
| 36 | 90 | 3.7 | 1172 | 9 | US-09-919-770-4 | Sequence 4, Appl1 |
| 37 | 90 | 3.7 | 1172 | 12 | US-10-301-822-203 | Sequence 203, App |
| 38 | 90 | 3.7 | 1172 | 15 | US-10-060-036-171 | Sequence 171, App |
| 39 | 90 | 3.7 | 1172 | 15 | US-10-020-141-14 | Sequence 14, Appl |
| 40 | 90 | 3.7 | 1172 | 15 | US-10-017-724-2 | Sequence 2, Appl1 |
| 41 | 89.5 | 3.7 | 561 | 15 | US-10-156-761-12820 | Sequence 12820, A |
| 42 | 88 | 3.6 | 1172 | 10 | US-09-822-682-2 | Sequence 2, Appl1 |
| 43 | 88 | 3.6 | 4551 | 11 | US-09-793-708-1 | Sequence 1, Appl1 |
| 44 | 88 | 3.6 | 4551 | 12 | US-10-201-365-2 | Sequence 2, Appl1 |
| 45 | 88 | 3.6 | 4551 | 12 | US-10-160-539-1 | Sequence 1, Appl1 |

ALIGNMENTS

RESULT 1
US-09-996-223-1

; Sequence 1, Application US/09996223

; Patent No. US20020099195A1

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.

LaI, Preeti

Shah, Puryl

TITLE OF INVENTION: HUMAN CITRATE SYNTHASE HOMOLOG

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSD for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/996,223

FILING DATE: 27-NO. US20020099195A1-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/970,134

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0425 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX: <Unknown>

APPLICATION NUMBER: US/09/996, 223
 FILING DATE: 27-No. US20020099195a1-2001
 CLASSIFICATION: <unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/970.134
 FILING DATE: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PP-0425 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-855-0555
 TELEFAX: 650-845-4166
 TELEX: <unknown>
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 464 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 164419
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 US-09-996-223-3
 Query Match 96.0%; Score 2339; DB 9; Length 464;
 Best Local Similarity 96.1%; Pred. No. 3.3e-227;
 Matches 446; Conservative 7; Mismatches 11; Gaps 0;


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; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 42562
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC020904.3
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 6.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.8
; OTHER INFORMATION: EST_HUMAN HIT: BE901274.1, EVALUATE 1.00e-58
; OTHER INFORMATION: SWISSPROT HIT: 075390, EVALUATE 1.00e-61
US-09-864-761-42562

Query Match          23.4%; Score 571; DB 9; Length 116;
Best Local Similarity 92.2%; Pred. No. 1.2e-49;
Matches 107; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

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OY 154 MLDNPTMLHPMSQSAVAVTALNSNFPARAAGISRTKYMELIYEDSMDIAKLPVCA 213
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DB 1 MLDNPTMLHPMSQSAVAVTALNSNFPARAAGISRTKYMELIYEDSMDIAKLPVCA 60

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OY 214 AKIYRNLYREGSGIGALDSNLDWSHNFTNMLGYTDHQPTELRLVLTJHSDHEGCGN 269.
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DB 61 AKIYRNLYREGSGIGALDSNLDWSHNFTNMLGYTDHQPTELRLVLTJHSDHEGCGN 116

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RESULT 4
US-09-738-626-6941

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; Sequence 6941, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIRO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 6941
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-6941

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Query Match 14.6%; Score 356; DB 10; Length 437;
Best Local Similarity 27.7%; Pred. No. 5e-27;
Matches 117; Conservative 83; Mismatches 149; Indels 74; Gaps 18;

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OY 120 FWLVLTGHIPTREOVSWLSKEMAKRAALPSHVVTMLDNFPTNMLHPMSQSAVAVTALNS 179
      |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 95 SYLLNGELPPDDELHKFNDEIRHHTLLDEDEKSFQNFVPPDAHFMATLASSVILST-- 152

OY 180 NFARAAGISRTKYMELIYEDSMD-----LAKLPVCAKITYRNLYREGSG 226
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DB 153 -----TYODLNPDLDEADLDKATVTLAKKVPMLAA--YAHARRKCAP 192

OY 227 IGALDSNLDWSHNFTNML-GYTDHQP-----TELRLVLTJHSDHEGCVNSAHTSHLV 278
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DB 193 YWYPDNSLNARENFLRMHFGVPTPEYEIDPIWVKALDKL-LILHADHE-QNCSTSTVRMI 250

OY 279 GSALSDPLSLRAAMNGIAGPLHGLANOEVLWLTOLQKEGVKQVSDKLDIYTNLTNS 338
      |||.....|.....|.....|.....|.....|.....|.....|.....|
DB 251 GSAOANMVSJAGGINALSGPLHGGANQAVLEMLEDIKSNKSGATE--FMNKVKNKEDG 308

OY 339 GRVWPGYGAHLRKTDPRPYTCOREFA---LKHLPMDPFRKLAQLYKIVPVLLIEGCKAK 395
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DB 309 VRLM-GEGRHYRYKNTDPAALYKEFAHLEHLEHSGDLDLDAIKLEIA--LADDFYFSR 365

OY 396 NPWPVNDASHGVLLQYCGMTENMYTVLVGVSRALGVLA----QILMSRALGFLERPES 451
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OY 452 MST 454
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DB 422 VYT 424

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RESULT 5.
US-10-156-761-12864
; Sequence 12864, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:

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Db 98 DEGIRFGFSIPECOKLLPKAISGGEPLPEGLFWLLV 134

RESULT 8

US-09-912-020-324
Sequence 324, Application US/09912020
Patent No. US20020045592A1
GENERAL INFORMATION:
APPLICANT: Zyskind, Judith
APPLICANT: Ohlsen, Karl L.
APPLICANT: Trawick, John
APPLICANT: Forsyth, R. Allen
APPLICANT: Froelich, Jamie M.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: GENES IDENTIFIED AS REQUIRED FOR PROLIFERATION IN
FILE REFERENCE: ELITRA.001DVI
CURRENT APPLICATION NUMBER: US/09/912,020
PRIOR FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: 09/492,709
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/117,405
PRIOR FILING DATE: 1999-01-27
NUMBER OF SEQ ID NOS: 485
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 324
LENGTH: 427
TYPE: PRT
ORGANISM: E. Coli
US-09-912-020-324

Query Match 13.0%; Score 315.5; DB 9; Length 427;
Best Local Similarity 26.4%; Pred. No. 5.9e-23;
Matches 116; Conservative 76; Mismatches 160; Indels 87; Gaps 20;

QY 57 KTVVGQITVDMAGMGRM-----KGLVETSS-----VLDDDEGRF-RGFSIPECOKLL 105
Db 22 KGTLAGQVDYDIRTUGSKGVFTFDDGFTSTASCESKITFTIDDEGILLHRGEP--DGLA 78
QY 106 PKAKGGEPLPEGLFWLLVGTGHIPIPEQVSNLSKEMAKRAALPSHVVTMLDNFPTNLHPM 165
Db 79 TDSNYL-----VCYILLNGEKPRQEDYEKTYVTHHTMIHEQITLFLFAFRDSHPM 132
QY 166 SOLSAAVTALNSESFAARAQAQISRTKYWELIYEDSMD-----LIADLPV 212
Db 133 AVMGITGALAA-----FYHDSLDVNNPRHREIAFAFLLSKMPTM 172
QY 213 AAKIYRNLYREGSGIGALDSNLDMSHNTNMLGYTDHOFTELRL-----YLTHSDH 265
Db 173 AAMCK--YSTGQPFYVRNDLSYAGNFLNMFFSTPCPYEVNPLERAMDRIILLHADH 230
QY 266 EGVNVSANTSHLVGSALSADPYLSFAAANGLAGPLHGLANOEVWLTLQLO--KEVGKDV 323
Db 231 E-QNASTVTRTAGSSGANPFACIAGIASLWGRHGANEAALKMLEISISVKKHIFEV 289
QY 334 SDEKLARDYIMWTLSNGRVVPGYGAHVLKRTDPRYTCOREF--ALKHL-PNDPMFKLVAQ 379
Db 290 RRADKN-----DSFRLM-GFGHRYVKNYDPRATVMKETCHEVYKELGTDDLLLEVAME 342
QY 380 LKXIVPN--VLLEGGKAKNPVNDANSGVLLQYGMTENMYTYLVESVSLGVLAOLI 437
Db 343 LENTALNDPFIET--KKLYPNDEYSGIILKAMGPS-SMFTVIFAMARTVGIAH-- 395
QY 438 WS--RALTGFLPERKSMST 454
Db 396 WSEMHSDGMKTIARPROLYT 414

RESULT 9

US-09-815-242-11282
Sequence 11282, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 11282
LENGTH: 426
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-815-242-11282

Query Match 11.2%; Score 274; DB 9; Length 426;
Best Local Similarity 27.7%; Pred. No. 9.1e-19;
Matches 108; Conservative 72; Mismatches 144; Indels 66; Gaps 18;

QY 72 MRCKGLVETSSVLDDDEGIRFGFSIPECOKLLPKAKGGEPLPEGLFWLLVGTGHIPIE 131
Db 59 VNGKKGELY-----YRGHRT--EDLVAKKYVD-----YCKLLTGELPKN 97
QY 132 EOVSM-LSKEMAKRAALPSHVVTMLDNFPTNLHPMSOLSAAVTALNSESFAARAQGIS 190
Db 98 QDESLEFELRLHRSFVHESLNMFSAPPSVAHPMAKLSSGVSLST-----LYSTH 149
QY 191 RTKWELIYED-SMDLIKLPCVAKIYRNLYREGSGIGALDSNLDMSHNTNML-GY-- 246
Db 150 QNMHTTEEDYQTMARITAKIPTLAIACV--EYGAPLIYDIDARSYENTLFLMGRPY 207
QY 247 -----TDHOFTELRL-----YLTHSDHEGVNVSANTSHLVGSALSADPYLSFAAAMN 294
Db 208 SRLKHTTQGEVEITRPLEVEARDKILTLHADH--SQNASSTYVRNASTGVHNYAALISGIS 266
QY 295 GLAEPHGLANOEVWLTLQLO--KEVGKDVSDKLARDYIMWTLSNGRVVPGYGAHVLK 352
Db 267 ALMCHLHGAGANEKVLLQLEETIGDVKNVDKYIA--RVKD-----KNDNFKLMFGHRYVKS 319
QY 353 TDRPYTCOREFALK--HLNPDPMFKLVAOLKYKYPNVLL--EQQKAKNPVNDANSGV 407
Db 320 YDPRAKILK--GLDELHQQGVKMKDERSETIAAVEETALKDEXFIERNLVPNVDFSGT 377
QY 408 LLOYGGMTEMYTYLVESVSLGVLAOLI 437
Db 378 ILRLAKTI-PVRFPTPVYIGRTVGMCAOLL 406

RESULT 10

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US-09-815-242-5427
; Sequence 5427, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5427
; LENGTH: 367
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-5427
```

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Query Match 10.6%; Score 257.5; DB 9; Length 367;
Best Local Similarity 26.6%; Pred. No. 3.3e-17;
Matches 100; Conservative 71; Mismatches 156; Indels 49; Gaps 15;

QY 73 RGKAGLV-YETSVLDPEG-IRFRGFSIPCCQKILPRKAGGEPDPEGLFWLVTGHIPT 130
DB 1 RGLGEGVIAETKISSIIESOLTAYAGYDIDL-----AENAOFEFVIFILMNYRLPN 51

QY 131 EEOVSMLSKEMAKRALPISHVYTMLONEPT-NLHPMSOLSAAYTALNSESINFARAYAOGI 189
DB 52 EEBLAIHLKGLNDYMTLNPRVYTHFEERYVDHHPMTALRTSLSYT-----AHFDDP 103

QY 190 SRTKYWELLYEDSMOILAKLPCVAARIYRLYREGSGIGALDSNLDMSHNFMTMLG---Y 246
DB 104 AENESDENRERARMIOAKVASLVTAFAR--VRQDEKPELKPNDLSYANFLYMLGELP 161

QY 247 TDHQFELRLYLTTHSDHEGNAVSAHTSLVGSALSDPYLSFAAAMNGIAGLUGLANQ 306
DB 162 TDIE-VEAFNKALILHADHE-LNAsAFTARCASVSDMSYGIYAAGVSLKGPLHGGANE 219

QY 307 EVIWMVLTLQKEGKDVODEKLDYIMNTLNSGRVAVPGYGHAVLKRKTDPRTYTCOREFA-- 364
DB 220 QVMTMLS---ETG---STENVDAYLDEKFRANKOKWGFGRHYKKGDPRAKYLREMSQ 272

QY 365 -LKHLPNDPFKLVLAOLYKTIKIPVNLLEOGKAKNPWPVNAHSGVLLQYYGMEPM--NYT 421
DB 273 ITKDAGREELFEKSVMEK-----RMADEKGLINVDYSA---SVYHCEIPIHDLFT 322

QY 422 VLFVSRALGVLAQLI 437
DB 323 PIFAVRSAGMIHIL 338
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RESULT 11

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US-09-815-242-12621
; Sequence 12621, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12621
; LENGTH: 373
; TYPE: PRF
; ORGANISM: Staphylococcus aureus
US-09-815-242-12621
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Query Match 10.6%; Score 257.5; DB 9; Length 373;
Best Local Similarity 26.6%; Pred. No. 3.4e-17;
Matches 100; Conservative 71; Mismatches 156; Indels 49; Gaps 15;

QY 73 RGKAGLV-YETSVLDPEG-IRFRGFSIPCCQKILPRKAGGEPDPEGLFWLVTGHIPT 130
DB 6 RGLGEGVIAETKISSIIESOLTAYAGYDIDL-----AENAOFEFVIFILMNYRLPN 56

QY 131 EEOVSMLSKEMAKRALPISHVYTMLONEPT-NLHPMSOLSAAYTALNSESINFARAYAOGI 189
DB 57 EEBLAIHLKGLNDYMTLNPRVYTHFEERYVDHHPMTALRTSLSYT-----AHFDDP 108

QY 190 SRTKYWELLYEDSMOILAKLPCVAARIYRLYREGSGIGALDSNLDMSHNFMTMLG---Y 246
DB 109 AENESDENRERARMIOAKVASLVTAFAR--VRQDEKPELKPNDLSYANFLYMLGELP 166

QY 247 TDHQFELRLYLTTHSDHEGNAVSAHTSLVGSALSDPYLSFAAAMNGIAGLUGLANQ 306
DB 167 TDIE-VEAFNKALILHADHE-LNAsAFTARCASVSDMSYGIYAAGVSLKGPLHGGANE 224

QY 307 EVIWMVLTLQKEGKDVODEKLDYIMNTLNSGRVAVPGYGHAVLKRKTDPRTYTCOREFA-- 364
DB 225 QVMTMLS---ETG---STENVDAYLDEKFRANKOKWGFGRHYKKGDPRAKYLREMSQ 277

QY 365 -LKHLPNDPFKLVLAOLYKTIKIPVNLLEOGKAKNPWPVNAHSGVLLQYYGMEPM--NYT 421
DB 278 ITKDAGREELFEKSVMEK-----RMADEKGLINVDYSA---SVYHCEIPIHDLFT 327

QY 422 VLFVSRALGVLAQLI 437
DB 328 PIFAVRSAGMIHIL 343
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RESULT 12

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US-09-815-242-12906
; Sequence 12906, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trivick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12906
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12906

Query Match
Best Local Similarity 26.6%; Score 257.5; DB 9; Length 373;
Matches 100; Conservative 71; Mismatches 156; Indels 49; Gaps 15;

QY 73 GKMGLVYE---TSVLDPDDEGIRFRGFSIPECOKILPKAKGGEPLPEGLFMLVTGHIPT 130
DB 6 RGLGVIADTYAVSKVMPETNSLTVRGYAVEDLV-----ENCSEFEVYLLMHGEL 61
QY 131 EBYVSWLSKEMAKRAALPSHVVTMLDNFPT-NLHPMSQLSAAVTALNSESNEFARAYAOGI 189
DB 57 EEEIAHLKGLKLNQVYTMPLRPVYTHPEEYVTDHVVHPTALRTSLSYT-----AHFDPD 108
QY 190 SRTKWMELIYEDSMOLIAKLPVAAKIRNLYREGSGIGAIDSNLDMSHNFTNMG---Y 246
DB 109 AENEDDERRYERAKMTQAKVASLTYAFAR--VRQKEPLKPNPDLSYANFLYMLRGELP 166
QY 247 TDHPTFLRLYLTIHSDHEGNSAHTSHLYGSALSDPYLSFAAMGLAGPLHGLANO 306
DB 167 TDIE-YEAFNFKALLIHADHE-LMASAFARCAVSSLSMYSIGIVAAGSINGPLRGANE 224
QY 307 EYLVMLTQLOKEVGKDVDEKLDYIMNTLNSGRVYPGYGAIVLKRTPRTYTCQREFA-- 364
DB 225 QVMTMLS---EIG---SIENVDAYLDEKFAKDKVMGFGHVRVYKDGDPRAKYLREMSQO 277
QY 365 -LKHLPNDPMFKLVNQLKIVPNVLLBOGKAKNPMPANDASGVLLQYGMTEM--NYT 421
DB 278 ITKDGREELPEMSYMER-----RMAEEKGLIPNDVYSA---SVYHCMEIPIHDLFT 327
QY 422 VLEGVSRALGVLAQLI 437
DB 328 PIFAVSRSGWIAHTL 343

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US-09-738-626-4233
; Sequence 4233, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAMA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIRO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4233
; LENGTH: 383
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4233

Query Match
Best Local Similarity 24.3%; Score 256.5; DB 10; Length 383;
Matches 94; Conservative 81; Mismatches 147; Indels 65; Gaps 14;

QY 73 GKMGLVYE---TSVLDPDDEGIRFRGFSIPECOKILPKAKGGEPLPEGLFMLVTGHI 128
DB 11 KGLGVIADTYAVSKVMPETNSLTVRGYAVEDLV-----ENCSEFEVYLLMHGEL 61
QY 129 PTEBYVSWLSKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAVTALNSESNEFARAYAOG 188
DB 62 PTAQOLAEFNEGRNSYRSLDGLISLHSLPKRAHPDMVMTAVSYM-----G 109
QY 189 ISRFKYW---ELIYEDSMOLIAKLPVAAKIRNLYREGSGIGAIDSNLDMSHNFTNML 244
DB 110 TKDSEYFTTDSHKKVYHTLLAQLPVLADIR--RKGDIITAPDSKSYAENLMSV 167
QY 245 GYT-----DHQFTFLRLYLTIHSDHEGNSAHTSHLYGSALSDPYLSFAAAMN 294
DB 168 FGTGESPAASNADVRDEFS--LIIYAEH-SFNASFTFARVITSTKSDVYSATIGAIG 223
QY 295 GIAGPLHGLANDEVVLMLTQLOKEVGKDVDEKLDYIMNTLNSGRVYPGYGAIVLKRTPD 354
DB 224 ALKGPLHGCAGNEFVHTMLAID-----DPNKAAMVIMNLDNNVVMGFGHRYKKRGD 276
QY 355 PRYTQO-----REFALKHLPNPDMFKLVNQLKIVPNVLLBOGKAKNPMPANDASGVLLQ 410
DB 277 SRVPSMEKSFRELARHNGE---KWVA-MYENMDADARIGIR---PNIDFPRAGRAYH 328
QY 411 YYGMTENMYVTVLEGVSRALGVLAQLI 437
DB 329 LLGF-PVDFEPLFVIARVAGWTIAHV 354

```

APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 9964
LENGTH: 388
TYPE: PRN
ORGANISM: Streptomyces avermitilis
US-10-156-761-9964

Query Match 9.98; Score 240.5; DB 15; Length 388;
Best Local Similarity 24.18; Pred. No. 1.9e-15;
Matches 98; Conservative 67; Mismatches 172; Indels 69; Gaps 16;

59 VVGQITVDMYGGKRGKGLYETSVLDPEGIFRFGFSIPECKLPRKAGGEPLPEG 118
17 LAGVYVDTSLGDRGLEGFYH-----YKQYSAVE---LAQTRGEED----- 55
QY 119 LFWLLVYTHIPTREQ-----VSLSKEMAKRALPSSHVVTMLDNPPTMLHPMSOL 168
DB 56 VVHLMVHGEPLDPAQRAVFTARFALRLPD--GVRAITLPAVAAA-----AGRSGLAGL 108
QY 169 SAAVTALNSESFRATAAGISRTKYWEILIYEDSMILAKPCVAAKTYRNLREGSGIG 228
DB 109 RTALSLGAAGKGFPPYV--DIDR-----EORRADTVMAAAPTLLTA-----LVRLGGGLD 158
QY 229 AID--SNLDWSHNTNML--GYTDHOFTELRLVLTJHSDHEGNSAHTSHLVGSALSD 284
DB 159 PVREDELSTAAANTLYMLTSSPPAARTRAIEQYLITIDH--GFNASTFAARYTTSIGAD 217
QY 285 PYLSFAAMNGLAGPLHGLANQEVYLVLTQKEVGVDSDEKLRYIWMTLNSGRVVP 344
DB 218 VAAALVGVAGVLSGLPHGAPSRALDPLAIG-----TPERDSWIRREVLAGDRIMG 270
QY 345 YGHAIVLEKTPRTYCCQEFALKHLPNPMEKLVLAQLKYIPNVYLLEGKAKNPVND 404
DB 271 FGHVYVTEDEPRSMGLVAEQF--GGPLVDFAVEVRRHVEALIAELKPGRELHTNVEFY 328
QY 405 SGVLLQYTGTEMNYYTVLFGVSRALGVLAQLIWSRALGPFLEPRK 450
DB 329 AGVVMELCGILPR-EMFTPTFAARVVG-----WSANILQCAEDPK 367

RESULT 15
US-09-738-626-4273
Sequence 4273, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, MAKIO
APPLICANT: SENOH, AKIHIO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 4273
LENGTH: 394
TYPE: PRN
ORGANISM: Corynebacterium glutamicum
US-09-738-626-4273

Query Match 9.78; Score 237.5; DB 10; Length 394;
Best Local Similarity 23.18; Pred. No. 3.9e-15;
Matches 90; Conservative 74; Mismatches 155; Indels 71; Gaps 16;

73 RGKKGLEYE-----TSVLDPEGIFRFGFSIPECKLPRKAGGEPLPEGFLVLTGHT 128
DB 21 KGLNGVSDYTSISKWPESSNLTNYGTAVEDLV-----ENCSEFEVITLWFGEL 71
QY 129 PTEBOVSLSKEMAKRALPSSHVVTMLDNPPTMLHPMSOLSAAVTALNS-----ESN 180
DB 72 PTEEQLETFNTGTSYRSYSLDAGLSLSLSPNCHPMDVLTAVSYMGTFDPDPPTRAD 131
QY 181 FARAYAGISRTKYWEILIYEDSMILAKPCVAAKTYRNLREGSGIGATDSNLSHNF 240
DB 132 HIRSLGH-----NLALQPLMVVAMDIR--RSGEETIAPDHKKGIASNF 173
QY 241 TNNMGYTD-----HOFTELRLVLTJHSDHEGNSAHTSHLVGSALSDPYLSFAA 292
DB 174 LSNVFGNDGVSANSADIDFER-SLITAEH-SFNASTFSAKYVTSRSDYSAITGA 231
QY 293 MNGIPLHGLANQEVYLVLTQKEVGVDS--EKLRYIWMTLNSGRVVPYGHAVLR 351
DB 232 IGALKGPLHGCANE--FVMTML-----DIDDPNNAADMWKGALDKRERIMGFGRVYK 283
QY 352 KTDPRY-----TCQREFALKLPNDPMEKLVLAQLKYIPNVYLLEGKAKNPVND 407
DB 284 NGDSRVPSMEKSMRSLAARHGG--KVV-HMYESQVEARITGK---PMLDEPAG 335
QY 408 LQYTGTEMNYYTVLFGVSRALGVLAQLI 437
DB 336 AYTMIGF-PVDFFTPLFLARVSGWTAHIV 364

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Job time: 64 secs

Check
LP

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OM protein - protein search, using sw model

Run on: September 5, 2003, 20:06:12; Search time 29 seconds
(without alignments)
679.892 Million cell updates/sec

Title: US-09-996-223-1
Perfect score: 2436
Sequence: 1 MALTTAARLTGKNAQLV.....ERPKSMTEGLMKFVDSKSG 466

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued_Patents_AA:
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2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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6: /cgn2_6/ptodata/1/1aa/Backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----------------------|-------------------|
| 1 | 2436 | 100.0 | 466 | US-08-970-134-1 | Sequence 1, Appl |
| 2 | 2339 | 96.0 | 464 | US-08-970-134-3 | Sequence 3, Appl |
| 3 | 338 | 13.9 | 431 | US-09-252-991A-25969 | Sequence 25969, A |
| 4 | 314 | 12.9 | 424 | US-09-328-352-4187 | Sequence 4187, Ap |
| 5 | 259 | 10.6 | 386 | US-09-134-001C-3770 | Sequence 3770, Ap |
| 6 | 234.5 | 9.6 | 390 | US-09-252-991A-29273 | Sequence 29273, A |
| 7 | 217 | 8.9 | 391 | US-09-328-352-4861 | Sequence 4861, Ap |
| 8 | 100 | 4.1 | 1118 | US-09-585-173B-36 | Sequence 36, Appl |
| 9 | 96 | 3.9 | 1447 | US-09-376-330-17 | Sequence 17, Appl |
| 10 | 94.5 | 3.9 | 3665 | US-08-222-617A-13 | Sequence 13, Appl |
| 11 | 94.5 | 3.9 | 3712 | US-08-222-617A-4 | Sequence 4, Appl |
| 12 | 94.5 | 3.9 | 3712 | US-08-222-617A-25 | Sequence 25, Appl |
| 13 | 92 | 3.8 | 1705 | US-08-669-785-4 | Sequence 4, Appl |
| 14 | 91 | 3.7 | 353 | US-09-252-991A-22881 | Sequence 22881, A |
| 15 | 90 | 3.7 | 1172 | US-08-313-288B-19 | Sequence 19, Appl |
| 16 | 89 | 3.7 | 1489 | US-08-669-785-2 | Sequence 2, Appl |
| 17 | 89 | 3.7 | 1706 | US-08-669-785-2 | Sequence 2, Appl |
| 18 | 89 | 3.7 | 1794 | US-09-328-352-5522 | Sequence 32058, A |
| 19 | 88 | 3.6 | 269 | US-09-252-991A-32058 | Sequence 32058, A |
| 20 | 88 | 3.6 | 459 | US-09-320-871-2 | Sequence 2, Appl |
| 21 | 88 | 3.6 | 912 | US-09-320-871-2 | Sequence 2, Appl |
| 22 | 88 | 3.6 | 4551 | US-09-141-908-2 | Sequence 1, Appl |
| 23 | 88 | 3.6 | 4551 | US-09-657-440-1 | Sequence 31, Appl |
| 24 | 88 | 3.6 | 4551 | US-09-105-537-31 | Sequence 6, Appl |
| 25 | 88 | 3.6 | 4613 | US-09-105-537-6 | Sequence 7, Appl |
| 26 | 88 | 3.6 | 11877 | US-09-894-698-7 | |
| 27 | 87.5 | 3.6 | 461 | US-09-894-698-7 | |

| | | | | | |
|----|------|-----|------|----------------------|-------------------|
| 28 | 87.5 | 3.6 | 483 | US-09-894-698-2 | Sequence 2, Appl |
| 29 | 87.5 | 3.6 | 888 | US-08-953-492-2 | Sequence 2, Appl |
| 30 | 87.5 | 3.6 | 988 | US-08-286-819A-19 | Sequence 19, Appl |
| 31 | 87.5 | 3.6 | 988 | US-08-980-357-19 | Sequence 19, Appl |
| 32 | 87.5 | 3.6 | 999 | US-08-473-553A-5 | Sequence 5, Appl |
| 33 | 87 | 3.6 | 1031 | US-09-585-173B-40 | Sequence 40, Appl |
| 34 | 87 | 3.6 | 1168 | US-08-448-170-6 | Sequence 6, Appl |
| 35 | 87 | 3.6 | 1168 | US-08-561-803-8 | Sequence 8, Appl |
| 36 | 86.5 | 3.6 | 700 | US-07-862-588B-2 | Sequence 2, Appl |
| 37 | 86 | 3.5 | 635 | US-08-873-475-43 | Sequence 43, Appl |
| 38 | 86 | 3.5 | 659 | US-08-136-277-3 | Sequence 3, Appl |
| 39 | 86 | 3.5 | 659 | US-08-479-403-3 | Sequence 3, Appl |
| 40 | 86 | 3.5 | 659 | US-08-835-734-3 | Sequence 3, Appl |
| 41 | 86 | 3.5 | 679 | US-09-252-991A-29548 | Sequence 29548, A |
| 42 | 85.5 | 3.5 | 552 | US-09-801-191A-6 | Sequence 6, Appl |
| 43 | 85.5 | 3.5 | 702 | US-09-328-352-8176 | Sequence 8176, Ap |
| 44 | 85.5 | 3.5 | 828 | US-09-107-532A-4191 | Sequence 4191, Ap |
| 45 | 85.5 | 3.5 | 1183 | US-08-447-031A-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-970-134-1
; Sequence 1, Application US/08970134
; Patent No. 6323328
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN CITRATE SYNTHASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,134
; FILING DATE: Herewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0425 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ENDCMOT03
; CLONE: 2171653
; US-08-970-134-1
Query Match 100.0%; Score 2436; DB 4; Length 466;

Best Local Similarity 100.0%; Pred. No. 2,8e-242; Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALTTAARLLGTRKNSCLVLAARHNASSTNLKDLADLIPREQARITFRQOHGTVV 60
   1 MALTTAARLLGTRKNSCLVLAARHNASSTNLKDLADLIPREQARITFRQOHGTVV 60
Db 1 MALTTAARLLGTRKNSCLVLAARHNASSTNLKDLADLIPREQARITFRQOHGTVV 60
QY 61 GQITVDMYGGMRGKGLVETSVLPDDEGIRFRGYSIPECOKLLPKAGGEEPLPEGIF 120
   61 GQITVDMYGGMRGKGLVETSVLPDDEGIRFRGYSIPECOKLLPKAGGEEPLPEGIF 120
Db 61 GQITVDMYGGMRGKGLVETSVLPDDEGIRFRGYSIPECOKLLPKAGGEEPLPEGIF 120
QY 121 WLVTGHIPTPEEOVSWLSKEMAKRALPSHVVTMLDNFPTNLHPMSQLSAAVTALESSE 180
   121 WLVTGHIPTPEEOVSWLSKEMAKRALPSHVVTMLDNFPTNLHPMSQLSAAVTALESSE 180
Db 121 WLVTGHIPTPEEOVSWLSKEMAKRALPSHVVTMLDNFPTNLHPMSQLSAAVTALESSE 180
QY 181 FARAYAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
   181 FARAYAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
Db 181 FARAYAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
QY 241 TNNLGYTDHOFTELRLYLTIIHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
   241 TNNLGYTDHOFTELRLYLTIIHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
Db 241 TNNLGYTDHOFTELRLYLTIIHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
QY 301 HGLANOEVWLWLOLQKEVGKDVSDKLRDIYNNLTNSGRVYPGCGHAYLRKTDPRYTQ 360
   301 HGLANOEVWLWLOLQKEVGKDVSDKLRDIYNNLTNSGRVYPGCGHAYLRKTDPRYTQ 360
Db 301 HGLANOEVWLWLOLQKEVGKDVSDKLRDIYNNLTNSGRVYPGCGHAYLRKTDPRYTQ 360
QY 361 REFALKHLPNDPMEKLVLAOLYKIVPNVLEOGKAKNPWNVDAHSGLVLLQYGMTENNY 420
   361 REFALKHLPNDPMEKLVLAOLYKIVPNVLEOGKAKNPWNVDAHSGLVLLQYGMTENNY 420
Db 361 REFALKHLPNDPMEKLVLAOLYKIVPNVLEOGKAKNPWNVDAHSGLVLLQYGMTENNY 420
QY 421 TVLFVSRALGVLAOLIWSRALGFPLERPKSMSTEGIMKFFVDSK 466
   421 TVLFVSRALGVLAOLIWSRALGFPLERPKSMSTEGIMKFFVDSK 466
Db 421 TVLFVSRALGVLAOLIWSRALGFPLERPKSMSTEGIMKFFVDSK 466

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RESULT 2

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US-08-970-134-3
; Sequence 3, Application US/08970134
; Patent No. 6323328
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN CITRATE SYNTHASE HOMOLOG
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/970,134
; FILING DATE: Herewith.
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0425 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166

```

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; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 164419
; US-08-970-134-3

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Query Match 96.0%; Score 2339; DB 4; Length 464;

Best Local Similarity 96.1%; Pred. No. 2,8e-232; Matches 446; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

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QY 1 MALTTAARLLGTRKNSCLVLAARHNASSTNLKDLADLIPREQARITFRQOHGTVV 60
   1 MALTTAARLLGTRKNSCLVLAARHNASSTNLKDLADLIPREQARITFRQOHGTVV 60
Db 1 MALTTAARLLGTRKNSCLVLAARHNASSTNLKDLADLIPREQARITFRQOHGTVV 60
QY 61 GQITVDMYGGMRGKGLVETSVLPDDEGIRFRGYSIPECOKLLPKAGGEEPLPEGIF 120
   61 GQITVDMYGGMRGKGLVETSVLPDDEGIRFRGYSIPECOKLLPKAGGEEPLPEGIF 120
Db 61 GQITVDMYGGMRGKGLVETSVLPDDEGIRFRGYSIPECOKLLPKAGGEEPLPEGIF 120
QY 121 WLVTGHIPTPEEOVSWLSKEMAKRALPSHVVTMLDNFPTNLHPMSQLSAAVTALESSE 180
   121 WLVTGHIPTPEEOVSWLSKEMAKRALPSHVVTMLDNFPTNLHPMSQLSAAVTALESSE 180
Db 121 WLVTGHIPTPEEOVSWLSKEMAKRALPSHVVTMLDNFPTNLHPMSQLSAAVTALESSE 180
QY 181 FARAYAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
   181 FARAYAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
Db 181 FARAYAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLREGSGIGALDSNLDMSHNF 240
QY 241 TNNLGYTDHOFTELRLYLTIIHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
   241 TNNLGYTDHOFTELRLYLTIIHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
Db 241 TNNLGYTDHOFTELRLYLTIIHSDHEGNSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
QY 301 HGLANOEVWLWLOLQKEVGKDVSDKLRDIYNNLTNSGRVYPGCGHAYLRKTDPRYTQ 360
   301 HGLANOEVWLWLOLQKEVGKDVSDKLRDIYNNLTNSGRVYPGCGHAYLRKTDPRYTQ 360
Db 301 HGLANOEVWLWLOLQKEVGKDVSDKLRDIYNNLTNSGRVYPGCGHAYLRKTDPRYTQ 360
QY 361 REFALKHLPNDPMEKLVLAOLYKIVPNVLEOGKAKNPWNVDAHSGLVLLQYGMTENNY 420
   361 REFALKHLPNDPMEKLVLAOLYKIVPNVLEOGKAKNPWNVDAHSGLVLLQYGMTENNY 420
Db 361 REFALKHLPNDPMEKLVLAOLYKIVPNVLEOGKAKNPWNVDAHSGLVLLQYGMTENNY 420
QY 421 TVLFVSRALGVLAOLIWSRALGFPLERPKSMSTEGIMKFFVDSK 464
   421 TVLFVSRALGVLAOLIWSRALGFPLERPKSMSTEGIMKFFVDSK 464
Db 421 TVLFVSRALGVLAOLIWSRALGFPLERPKSMSTEGIMKFFVDSK 464

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RESULT 3

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US-09-252-991A-25969
; Sequence 25969, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 25969
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-25969

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Query Match 13.9%; Score 338; DB 4; Length 431;
Best Local Similarity 27.0%; Pred. No. 4.4e-26;

RESULT 6

Db 588 TVGRNIEDVYR-GSKGIAD-----VELL-----ROITEASGATTFEVERTNNKG 634
QY 270 ---VSANTSHLVGSLSDPYLSFAAAMNGLAGPLHGLANOEVLWLOLOKEVGDVSD 325
Db 635 QVVDVYTNKLSLWGLGSLSPWQHLSTKTKFIRADREKL---RLLFFLGECLKLI---VAD 689
QY 326 EKLRYD IMNTLNSGRVAVPGYHAUVRKTDPRYTCOREPAL--KHLRNDPMFKLVLAOLYKI 383
Db 690 NELGS-LKLALEGSYVEPCPGDPIRNPKVLPRTGNINHLDPQALPTTAAALKSA-----KI 744
QY 384 VPNVLLEOGKAKN--PWRVVDHSGVLLQYGMTEMNYYTVFGVSRALGVLAOLIW 438
Db 745 IVDRLEROKYDNGSKYPET-----IALVWGTDNIKTY-----LAQYLIW 787

RESULT 9
US-09-376-330-17
Sequence 17, Application US/09376330
Patent No. 6399321
GENERAL INFORMATION:
APPLICANT: Tessier, Daniel C.
APPLICANT: Dignard, Daniel
APPLICANT: Bergeron, John J.M.
APPLICANT: Thomas, David Y.
TITLE OF INVENTION: Method for screening for
TITLE OF INVENTION: UDP-glucose:glycoprotein glucosyltransferase (UGGT) activity
TITLE OF INVENTION: and nucleic acid encoding for UGCT
FILE REFERENCE: 2139-9*us*
CURRENT APPLICATION NUMBER: US/09/376,330
CURRENT FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 1447
TYPE: prt
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: S. pombe UGCT
US-09-376-330-17

Query Match 3.9%; Score 96; DB 4; Length 1447;
Best Local Similarity 20.8%; Pred. No. 2.9;
Matches 103; Conservative 62; Mismatches 177; Indels 154; Gaps 23;

QY 10 LLGTFKNAS-CLVIAARHSAASSTNLKDLADLPKEQARITFRQGHCKTVVGOITVMM 68
Db 675 LIGSSNAKYSPWLVADFNKEGGLTSLDLADLLSENKDANMLIOEGKNHVPPLFAKL 734
QY 69 YGMRGMKGL-VYETSVLPDEGIRFRGFSIPECOKLPRKAGGEPPLPEGIFW-----L 122
Db 735 SSPKSSKHQELINSSSIDPSSGV--VNDMDKALKFLKSKAAVVKEL--GLTGCKSAL 789
QY 123 LVYGH-----IPEDOVSWLSK---EMAKRAALPSHVVTMLDNEPTN 161
Db 790 LLNGMICSFSVDSLNTADLMKQMEYDNLKSNLIGSSRRLKNSRAISFLSSYLKT 849
QY 162 LH--PMSQLS-----AAVTALNSESMPARAYAGIS-----RTKXW 195
Db 850 LESTPMSTSPTEKEKLEPPROFIYKLCVGNNATFETDPSKAYTOFAVLDPKSDOKW 909
QY 196 ELIYEDSMDLIAKLPVAAKIYRNLVREGSGIGALSDNLDNSHNTNMLGYTDHOFTEL 255
Db 910 SAI-----LEAVSKLNGVGRVRIHLPKOTLSEL-----PLT 940
QY 256 RLILTIHSDHSGGANSATSHLVGSALSDPYLSFAAAMNGLAGPLHGLANOEVL---VWL 312
Db 941 RFRYR-----SISAEPEFDALGHLEESYVEF---DNL--PADTLTLMDEIARDAM- 985
QY 313 TOLQKEVGKDVSEKLT-----RDYIMNTLNSGRVAVPGYHAUVRKTDPR----- 356
Db 986 TVMKQDVYDIDLFNKLKLEHTSBAEALDSHTAIYELKNT--LVQGSQEEFRKSPRGMOLK 1043
QY 357 -----YTCOREFALKHLRPN-----DPMFKLVLAOLYKI VPNVLLEOGK 393

Db 1044 LGNLTNSHTDTIVLSNLGY-----FOLKANGVLTLEPMGRSSQFEILS--LNKNS 1096
QY 394 AKNPPNNDAMSGVLL 409
Db 1097 YKDPQIVDSFEGVTL 1112

RESULT 10
US-08-222-617A-13
Sequence 13, Application US/08222617A
Patent No. 5882879
GENERAL INFORMATION:
APPLICANT: Veenstra, Annemarie E.
APPLICANT: Martin, Juan F.
APPLICANT: Garcia, Bruno D.
APPLICANT: Gutierrez, Santiago
APPLICANT: Barredo, Jose L.
APPLICANT: Von Doehren, Hans
APPLICANT: Palissa, Harriet
APPLICANT: Van IJempt, Henk
TITLE OF INVENTION: A Method for Influencing Beta-Lactam
TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
TITLE OF INVENTION: Quantities of ACV Synthetase
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: McConnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,617A
FILING DATE: 04-APR-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 97,157
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 3665 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Acremonium chrysogenum
FEATURE:
NAME/KEY: Protein
LOCATION: 1..3665
OTHER INFORMATION: /label= ACVS
OTHER INFORMATION: /note= "ACV Synthetase from Acremonium
OTHER INFORMATION: chrysogenum; aa 1-3665"
US-08-222-617A-13

Query Match 3.9%; Score 94.5; DB 2; Length 3665;
Best Local Similarity 21.7%; Pred. No. 19;
Matches 63; Conservative 47; Mismatches 91; Indels 89; Gaps 15;

QY 60 VGOITVDMVGMGMKGLVYETSVLPDEGIRFRGFSIPECOKLPRKAGGEPPLPEG 119
Db 671 LGRADFOIKLNGIIEPEIESTLAMYP--GIR--ASTVSKLLSO--GQETTDH 722
QY 120 --FWLVTGHIPTPEOVSWLSKEWAKRAALPSHVVTMLDNEPTNHL-----PMSQLS 169

Db 723 VGYVDEBHIPEGDLISLEKK-LPRYWPRLV-QLAQPITNINGKADRALPAVEYA 780
QY 170 AAVT-----ALNSESNFARAYAGISRTKYWELIYED 201
Db 781 VAPTHKODGERGNQLESIDLAIWGNILSVPAODIGSESNEFRLGCHSIA-----829
QY 202 SMDLAKLPCVAKIYRNLYREGSGIGALDSNLDMSHNTNMLGYTDHOFTELRLYLI 261
Db 830 CIOIARV-----ROOLGOGITLLEEVFOFKTLRAAALLSEKYYKAS-----871
QY 262 HSDHEGNG-VSAHTSHLVGSA-----LSDPYLSFAAAMNGLAPLGLANO 306
Db 872 ----NCTNGVTNGTAHVNGHANGHVSYSVA-SSLOQGFV--YHSKNE 914

RESULT 11
US-08-222-617A-4
; Sequence 4, Application US/08222617A
; Patent No. 5882879
; GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Santiago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet
; APPLICANT: Montenegro, Eduardo P.
; TITLE OF INVENTION: A Method for Influencing Beta-Lactam
; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
; TITLE OF INVENTION: Quantities of ACV Synthetase
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,617A
; FILING DATE: 04-Apr-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 97,157
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3712 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; NAME/KEY: Modified-site
; LOCATION: 2555
; OTHER INFORMATION:
; OTHER INFORMATION: /note="Xaa-Ala or Ser"
US-08-222-617A-4

Query Match 3.9%; Score 94.5; DB 2; Length 3712;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 63; Conservative 47; Mismatches 91; Indels 89; Gaps 15;
QY 60 VGOITVDMYGMKMGKGLVETSVDPDEGIRFRGFSIPECOKLLPKAKGEEPLPEGL 119
Db 671 LGRADQIKLRIGIRIEPGEIESTLAMP--GIR---ASIVSKKLSQ---GQETIQDHL 722
QY 120 --FWLVTGHIPTIEGVSWLSKEMAKRALPSHVYTMIDNFPYLNH-----PMSQLS 169

Db 723 VGYVDEBHIPEGDLISLEKK-LPRYWPRLV-QLAQPITNINGKADRALPAVEYA 780
QY 170 AAVT-----ALNSESNFARAYAGISRTKYWELIYED 201
Db 781 VAPTHKODGERGNQLESIDLAIWGNILSVPAODIGSESNEFRLGCHSIA-----829
QY 202 SMDLAKLPCVAKIYRNLYREGSGIGALDSNLDMSHNTNMLGYTDHOFTELRLYLI 261
Db 830 CIOIARV-----ROOLGOGITLLEEVFOFKTLRAAALLSEKYYKAS-----871
QY 262 HSDHEGNG-VSAHTSHLVGSA-----LSDPYLSFAAAMNGLAPLGLANO 306
Db 872 ----NCTNGVTNGTAHVNGHANGHVSYSVA-SSLOQGFV--YHSKNE 914

RESULT 12
US-08-222-617A-25
; Sequence 25, Application US/08222617A
; Patent No. 5882879
; GENERAL INFORMATION:
; APPLICANT: Veenstra, Annemarie E.
; APPLICANT: Martin, Juan F.
; APPLICANT: Garcia, Bruno D.
; APPLICANT: Gutierrez, Santiago
; APPLICANT: Barredo, Jose L.
; APPLICANT: Von Doehren, Hans
; APPLICANT: Palissa, Harriet
; APPLICANT: Montenegro, Eduardo P.
; TITLE OF INVENTION: A Method for Influencing Beta-Lactam
; TITLE OF INVENTION: Antibiotic Production and for Isolation of Large
; TITLE OF INVENTION: Quantities of ACV Synthetase
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,617A
; FILING DATE: 04-Apr-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; REFERENCE/DOCKET NUMBER: 97,157
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3712 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-222-617A-25

Query Match 3.9%; Score 94.5; DB 2; Length 3712;
Best Local Similarity 21.7%; Pred. No. 20;
Matches 63; Conservative 47; Mismatches 91; Indels 89; Gaps 15;
QY 60 VGOITVDMYGMKMGKGLVETSVDPDEGIRFRGFSIPECOKLLPKAKGEEPLPEGL 119
Db 671 LGRADQIKLRIGIRIEPGEIESTLAMP--GIR---ASIVSKKLSQ---GQETIQDHL 722
QY 120 --FWLVTGHIPTIEGVSWLSKEMAKRALPSHVYTMIDNFPYLNH-----PMSQLS 169
Db 723 VGYVDEBHIPEGDLISLEKK-LPRYWPRLV-QLAQPITNINGKADRALPAVEYA 780
QY 170 AAVT-----ALNSESNFARAYAGISRTKYWELIYED 201

Db 781 VAPTHKODGERGNOLESDLAIAWGNILSVPAODIGSESNFRIGHSIA----- 829
Qy 202 SMDLAKLPCVAKIYRNLREGSGIGADSNLMDSHNTNMLGTDHOFTELRLYLTI 261
Db 830 CIQLARY-----ROOQOGITLLEEVFOFKTLRAMAALLSEYTKAS----- 871
Qy 262 HSDHEGCGN-VSARTSHLYGSA-----LSDPYLSFAAAMNGIAGPLIGLANO 306
Db 872 ---NGTNGVTNGTAHVNGHANGVSDSYA--SSLOQCFV--YHSLKNE 914
RESULT 13
US-08-669-785-4
; Sequence 4, Application US/08669785
; Patent No. 6309648
; GENERAL INFORMATION:
; APPLICANT: Betsou, Fotini
; APPLICANT: Sebou, Peter
; APPLICANT: Guiso, Nicole
; TITLE OF INVENTION: Protective Epitopes Of Adenyl
; TITLE OF INVENTION: Cyclase-Haemolysin(AC-HLY) Their Application To
; TITLE OF INVENTION: The Treatment Or To The Prevention Of Bordetella Infections.
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Finegan, Henderson, Farabow, Garrett & Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/669,785
; FILING DATE: 27-JUN-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 02356, 0072-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1705 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
; US-08-669-785-4
Query Match 3.8%; Score 92; DB 4; Length 1705;
Best Local Similarity 22.2%; Pred. No. 9.8;
Matches 94; Conservative 58; Mismatches 153; Indels 118; Gaps 23;
Qy 7 AARLIGTK---NASCLVLAARHASASTNLKDLADLIPKQARIKTFROQHGKTVVQ 62
Db 768 ASSVIGVOTTEISKSALELAITGNADNLKSDAVFD-----RFQGERVAGQ 815
Qy 63 -ITVDMMYG--MRMKG---LYETSVLPDDEGIRRGSIPECQKLLPKAKGGEPL 115
Db 816 PVLVDVAAGGIDIASRKGERPALTEITPLAAGEQRR-----TKTKGS-- 860
Qy 116 PEGLEFLVLTGHIPEQOVSWLSKEMAKRALP--SHVYMLDNFPTNLHPMSQLSAAYTA 174
Db 861 -EFFTFEIVG-----KQDRRIKRGADDTITDLAKVYSQ-----VDANGVLKHSIKLEV 910
Qy 175 LNSE-----SNFARAY---AOGISRTKYWELIYEDSMDLAKLPCVAKIYR----- 218

Db 911 IGGDDDDVVLANASRIHVDGAGTNTVSYAALGRDSDI-----TVSADGERFVNRQL 963
Qy 219 ---NLYREG-----SGICAIDSNLMDSHNTNMLGTDHOFTELRLYLTIHSDHEGCV 270
Db 964 NNANVYRRGVATQKAYGKRTENVQY RHELARVG---QLVEVPTLHVHVIIGAGND 1019
Qy 271 S-----AHTSHVGSALSDPYLSFAAAMNGIAG-----PLHGLANQEVL---VM/TOLO 316
Db 1020 SITGNAHDFLAGGA-GDDRDLGGAGNDITLVGEGHNTVYVGAGDVFLODLGVMSND 1078
Qy 317 KEVGKDY-----SDEKLRDYIWNLTNSGRVPGYGHAVLRK--TDPRYTCQREFALK 367
Db 1079 GGAGVDYTKVYNVHQPSEERLE-----RMGDTGIHADLOKCTVEKWPALNLFSDH 1128
Qy 368 LPN 370
Db 1129 VKN 1131
RESULT 14
US-09-252-991A-22881
; Sequence 22881, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUSINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22881
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-252-991A-22881
Query Match 3.7%; Score 91; DB 4; Length 353;
Best Local Similarity 23.6%; Pred. No. 0.91;
Matches 54; Conservative 32; Mismatches 77; Indels 66; Gaps 12;
Qy 3 LITAAARLGT--KNASCLVLAARHASASTNLKDLADLIPKQARIKTFROQHGKTVVQ 61
Db 104 MLAASLLCGTLKFDGLLVQARSGA-----VPLMVECSSDRQVRG---LA 148
Qy 62 QITVDMYGMGMKGLVYE---TSVLPDDEGIRRGF-----SIPECQKLLPKAKGE 112
Db 149 RYSAESI-GADGAGMOELMPEGVLTTPVAGQRYQGVALBQVLAEC---LSNYFASS 204
Qy 113 EPLPEGLFVLVTG-----HIPEQOVSWLSKEMAKRALP--SHVYMLDNFPTNLH 163
Db 205 EQLP--RRLWANAGRANGLLIQLQAPDR-----LKDEARASQHLITLADTL----- 253
Qy 164 PMSQLSAAVTALNSSENFARAYAGISRTKYWELIYEDSMDLAKPCV 212
Db 254 ---TAEBLLALDNETVLRILY-----HEETVRLFEPOPVL 285
RESULT 15
US-08-313-288B-19
; Sequence 19, Application US/08313288B
; Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, Thomas M. and Avihu Klar
; TITLE OF INVENTION: CLONING, EXPRESSION AND USES OF A
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:

ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,288B
FILING DATE: January 5, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 40028-A-PCT-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEFAX: (212) 391-0526
TELEX:
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1172 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-288B-19

Query Match 3.7%; Score 90; DB 1; Length 1172;
Best Local Similarity 21.1%; Pred. No. 8.5;
Matches 68; Conservative 44; Mismatches 112; Indels 98; Gaps 17;
QY 39 DLIPKBEAR-----IKTFROHGKTVYGQITVDMVGMGMKGLVETSVLDDPEGIRF 93
Db 61 DYIPVNAVADLSKITKIMROKEGFFLPAOLKOD--GKSRG-----TLALEGPELSQ 110
QY 94 RGFSLPCQKLLPKAKGGEPLPEGLFWLVGTGHIPTREQVSWLSKEMAKRAALPSHVT 153
Db 111 RQFEL-----VSNQPADTLDLTWIDGTRHVSLEDPVGLADSQW-----KNVTV 154
QY 154 MLDNFPNLIHPSQLSAVTAALS-----ESNFRAY-AQGISRTKW-----ELIY 199
Db 155 QVAGETYSLVHVGCDLIGPV-ALDEPEYEHQAERSRMYVAKGSARSHFRGLLQNVHLVF 213
QY 200 EDSW-DLIAKLPVAAKIYRNLYREGSGIGALDSNLD---WSHNFTNMLGYDHOFTL 254
Db 214 ENSVEDTLKKKCGOQ-----QGAELNNISENTETLRIGPHVTTEYVGPSSERPEV 265
QY 255 TRYLTISHDEGNGVSAHTSHLVGSALSDPYLSFAAAMNGLAGPLHGLANQEVLVWLQ 314
Db 266 CE-----RSCDELGNM-----VOELSG-LHVLVNO-----LSE 292
QY 315 LQEVGKDVSDKLRDIYIWNLT 336
Db 293 NLKRVSNQ-----NOFLWELI 308

Search completed: September 5, 2003, 20:11:25
Job time : 34 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2003, 20:06:07 ; Search time 101 Seconds
(without alignments)
1190.619 Million cell updates/sec

Title: US-09-996-223-1
Perfect score: 2436
Sequence: 1 MALLTAARLGTGNASCLV.....ERPKSMSTEGIMKRVDSKSG 466

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_todent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 2436 | 100.0 | 466 | 4 | Q96FZ8 |
| 2 | 2323 | 95.4 | 466 | 11 | Q8VHF5 |
| 3 | 2321 | 95.3 | 466 | 11 | Q9CZU6 |
| 4 | 2219 | 91.1 | 466 | 11 | Q9DAM4 |
| 5 | 1737.5 | 71.3 | 464 | 5 | Q9W401 |
| 6 | 1735 | 71.2 | 522 | 5 | Q8T477 |
| 7 | 1549 | 63.6 | 474 | 3 | Q8NKF2 |
| 8 | 1539.5 | 63.2 | 474 | 3 | Q8P8D6 |
| 9 | 1507 | 61.9 | 472 | 3 | Q9HFT1 |
| 10 | 1501.5 | 61.6 | 469 | 3 | Q9P688 |
| 11 | 1497.5 | 61.5 | 456 | 3 | Q8NJT0 |
| 12 | 1483.5 | 60.9 | 460 | 5 | Q8SSP7 |
| 13 | 1481.5 | 60.8 | 472 | 10 | Q9PUJ7 |
| 14 | 1480.5 | 60.8 | 437 | 10 | Q96544 |
| 15 | 1480.5 | 60.8 | 475 | 3 | Q9P4E3 |
| 16 | 1473.5 | 60.5 | 433 | 10 | Q9MID3 |

| | | | | | | |
|----|--------|------|-----|----|--------|--------------------|
| 17 | 1457.5 | 59.8 | 473 | 10 | Q946X8 | Q946X8 prunus pers |
| 18 | 1439 | 59.1 | 469 | 10 | Q24135 | Q24135 nicotiana t |
| 19 | 1396 | 57.3 | 264 | 4 | Q9BWM8 | Q9BWM8 homo sapien |
| 20 | 1377.5 | 56.5 | 493 | 10 | Q9XGN7 | Q9XGN7 oryza sativ |
| 21 | 1232 | 50.6 | 478 | 5 | Q95TZ4 | Q95TZ4 drosophila |
| 22 | 1158 | 47.5 | 460 | 8 | Q9TEM3 | Q9TEM3 emericella |
| 23 | 1108.5 | 45.5 | 339 | 10 | Q24259 | Q24259 populus bai |
| 24 | 1071 | 44.0 | 261 | 5 | Q8T9J9 | Q8T9J9 drosophila |
| 25 | 931.5 | 38.2 | 563 | 5 | Q816U7 | Q816U7 plasmodium |
| 26 | 685 | 28.1 | 138 | 6 | Q8KMY1 | Q8KMY1 bos taurus |
| 27 | 580 | 23.8 | 188 | 10 | Q8H9E3 | Q8H9E3 sesbania ro |
| 28 | 366.5 | 15.0 | 470 | 16 | Q8RQP3 | Q8RQP3 corynebacte |
| 29 | 346 | 14.2 | 429 | 16 | Q9R3P9 | Q9R3P9 streptomyce |
| 30 | 345.5 | 14.2 | 427 | 17 | Q9J0X0 | Q9J0X0 neisseria m |
| 31 | 341 | 14.0 | 373 | 17 | Q974S5 | Q974S5 sulfolobus |
| 32 | 339.5 | 13.9 | 514 | 10 | Q9LXS6 | Q9LXS6 arabidopsis |
| 33 | 338 | 13.9 | 509 | 10 | Q9S3H7 | Q9S3H7 arabidopsis |
| 34 | 336.5 | 13.8 | 377 | 2 | Q9LXC9 | Q9LXC9 thermus the |
| 35 | 335.5 | 13.8 | 412 | 2 | Q9KJF8 | Q9KJF8 rickettsia |
| 36 | 335.5 | 13.8 | 429 | 16 | Q8F801 | Q8F801 leptospira |
| 37 | 333 | 13.7 | 413 | 2 | Q9F111 | Q9F111 rickettsia |
| 38 | 332.5 | 13.6 | 377 | 2 | Q8VLZ3 | Q8VLZ3 thermus aqu |
| 39 | 331.5 | 13.6 | 410 | 2 | Q9LAF3 | Q9LAF3 rickettsia |
| 40 | 331.5 | 13.6 | 410 | 2 | Q9LAF5 | Q9LAF5 rickettsia |
| 41 | 331.5 | 13.6 | 411 | 2 | Q8KWU7 | Q8KWU7 rickettsia |
| 42 | 331.5 | 13.6 | 431 | 16 | Q33066 | Q33066 mycobacteri |
| 43 | 331 | 13.6 | 413 | 2 | Q9F110 | Q9F110 rickettsia |
| 44 | 330.5 | 13.6 | 411 | 2 | Q594E9 | Q594E9 israeli tic |
| 45 | 330 | 13.5 | 411 | 2 | Q8KWU8 | Q8KWU8 rickettsia |

ALIGNMENTS

RESULT 1

Q96FZ8 ID Q96FZ8 PRELIMINARY; PRT; 466 AA.
AC Q96FZ8:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein FLJ90475 (EC 4.1.3.7) (Citrate synthase).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX NCBI_TaxID=9606;
RN [1]
RN [1] SEQUENCE FROM N.A.
RP STRAUSBERG R.;
RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RP Isoogl T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T., Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K., Masuno Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N., Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RA "NBD human cDNA sequencing project.";
RT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O + OXALOCETATE.
CC -I- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -I- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
DR EMBL: BC010106; AAH10106.1; -;
DR EMBL: AK074956; BAC11314.1; -;
DR InterPro: IPR002020; Citrate_synth.
DR Pfam: PF00285; Citrate_synth. 1.
DR PRINTS: PR00143; CITRATESYNTHASE.
DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
KW Hypothetical protein; Lyase; Tricarboxylic acid cycle.
SQ SEQUENCE 466 AA; 51712 MW; 459CB29C0BA06997 CRC64;

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Query Match      100.0%; Score 2436; DB 4; Length 466;
Best Local Similarity 100.0%; Pred. No. 8.8e-190;
Matches 466; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MALLTAAARLGLGNKSNCLVLAARHNASASTNLKDLADLPKEQARITFRQOHKTYV 60
DB 1 MALLTAAARLGLGNKSNCLVLAARHNASASTNLKDLADLPKEQARITFRQOHKTYV 60
OY 61 GQITVDMYGMKGMKGLVETSVLDPDEGIRFRGSIPECOKLPRKAGGEEPLEGLE 120
DB 61 GQITVDMYGMKGMKGLVETSVLDPDEGIRFRGSIPECOKLPRKAGGEEPLEGLE 120
OY 121 WLLVTHIPIPEEYVSWLSKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAYTALNSEN 180
DB 121 WLLVTHIPIPEEYVSWLSKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAYTALNSEN 180
OY 181 FARAAGISIRKRYWELIYEDSMDLAKLPCVAAKIYRNLVREGSGIGADISLDMSHNF 240
DB 181 FARAAGISIRKRYWELIYEDSMDLAKLPCVAAKIYRNLVREGSGIGADISLDMSHNF 240
OY 241 TNNLGYTDHOFTELRLYLTIHSDHEGYNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
DB 241 TNNLGYTDHOFTELRLYLTIHSDHEGYNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
OY 301 HGLANDEVWLTLQLOKEVKDYSDEKLDYIWNITNSGRVVPYGYHAVALRKTDPRYTCQ 360
DB 301 HGLANDEVWLTLQLOKEVKDYSDEKLDYIWNITNSGRVVPYGYHAVALRKTDPRYTCQ 360
OY 361 REFALHLPNDPMPFKLVAOLYKIVPNVLEEGKAKNPWNVDAHSGVLLQYGMTMANY 420
DB 361 REFALHLPNDPMPFKLVAOLYKIVPNVLEEGKAKNPWNVDAHSGVLLQYGMTMANY 420
OY 421 TVLFGVSRAALGVLAOLIMSRALGFLEPRKSMSTEGIMKFDVDSKSG 466
DB 421 TVLFGVSRAALGVLAOLIMSRALGFLEPRKSMSTEGIMKFDVDSKSG 466

RESULT 2
ID 08VHF5 PRELIMINARY; PRT; 466 AA.
AC 08VHF5;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DE citrate synthase (EC 4.1.3.7).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Rossignol F., Jouanville L., Mounier R., Clottes E.;
RT "Rattus norvegicus citrate synthase cDNA.";
RL Submitted (DEC-2001) to the EMBL/GenBank/ODD databases.
CC -1- CATALYTIC ACTIVITY: CITRATE + COA -> ACETYL-COA + H(2)O +
CC OXALOACETATE.
CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
DR EMBL: AF61496; AAL6372.1; -
DR InterPro: IPR002020; Citrate_synth.
DR Pfam: PF00285; citrate_synth.
DR PRINTS: PR00143; CITRATSYNTHASE.
DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
KW Lyase; Tricarboxylic acid cycle.
SQ SEQUENCE 466 AA; 51866 MW; AF8D38379CD38124 CRC64;

Query Match      95.4%; Score 2323; DB 11; Length 466;
Best Local Similarity 94.6%; Pred. No. 1.4e-180;
Matches 441; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 1 MALLTAAARLGLGNKSNCLVLAARHNASASTNLKDLADLPKEQARITFRQOHKTYV 60

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DB 1 MALLTAAARLGLGNKSNCLVLAARHNASASTNLKDLADLPKEQARITFRQOHKTYV 60
OY 61 GQITVDMYGMKGMKGLVETSVLDPDEGIRFRGSIPECOKLPRKAGGEEPLEGLE 120
DB 61 GQITVDMYGMKGMKGLVETSVLDPDEGIRFRGSIPECOKLPRKAGGEEPLEGLE 120
OY 121 WLLVTHIPIPEEYVSWLSKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAYTALNSEN 180
DB 121 WLLVTHIPIPEEYVSWLSKEMAKRAALPSHVVTMLDNFPTNLHPMSQLSAAYTALNSEN 180
OY 181 FARAAGISIRKRYWELIYEDSMDLAKLPCVAAKIYRNLVREGSGIGADISLDMSHNF 240
DB 181 FARAAGISIRKRYWELIYEDSMDLAKLPCVAAKIYRNLVREGSGIGADISLDMSHNF 240
OY 241 TNNLGYTDHOFTELRLYLTIHSDHEGYNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
DB 241 TNNLGYTDHOFTELRLYLTIHSDHEGYNVSAHTSHLVGSALSDPYLSFAAAMNGLAGPL 300
OY 301 HGLANDEVWLTLQLOKEVKDYSDEKLDYIWNITNSGRVVPYGYHAVALRKTDPRYTCQ 360
DB 301 HGLANDEVWLTLQLOKEVKDYSDEKLDYIWNITNSGRVVPYGYHAVALRKTDPRYTCQ 360
OY 361 REFALHLPNDPMPFKLVAOLYKIVPNVLEEGKAKNPWNVDAHSGVLLQYGMTMANY 420
DB 361 REFALHLPNDPMPFKLVAOLYKIVPNVLEEGKAKNPWNVDAHSGVLLQYGMTMANY 420
OY 421 TVLFGVSRAALGVLAOLIMSRALGFLEPRKSMSTEGIMKFDVDSKSG 466
DB 421 TVLFGVSRAALGVLAOLIMSRALGFLEPRKSMSTEGIMKFDVDSKSG 466

RESULT 3
ID 09CZU6 PRELIMINARY; PRT; 464 AA.
AC 09CZU6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2002 (Tremblrel. 22, Last annotation update)
DE 2610511A05SRlx protein (EC 4.1.3.7) (Citrate synthase).
GN CS OR 2610511A05SRlx.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinsawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojibori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glass C., King B., Koehli H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schmitt L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazarrelli J., Mommaerts P.,
RA Nordone P., Ring B., Ringwald K., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Sone H., Shimano H., Yamada N.;
RT "murine citrate synthase, complete.";

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RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
 RN [3] SEQUENCE FROM N.A.
 RC Tissue-Kidney;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
 RN [4] SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC OXALACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 DR EMBL: AK012151; BAB28063.1; -
 DR EMBL: AB056479; BAB63945.1; -
 DR EMBL: BC013554; AAH13554.1; -
 DR EMBL: BC029754; AAH29754.1; -
 DR HSSP: P00889; 2CTS.
 DR MGD: MGI:88529; CS.
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth.
 DR PRINTS: PR00143; CITRATESNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
 KW Lyase; Tricarboxylic acid cycle.
 SO SEQUENCE 466 AA; 51736 MW; 710639871C31EED5 CRC64;

Query Match 95.3%; Score 2321; DB 11; Length 464;
 Best Local Similarity 94.4%; Pred. No. 2e-180;
 Matches 438; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OY 1 MALTTAARLLGKASCLVLAARHASASTNLKDLADLPKEQARIKTRQOHGKTVV 60
 DB 1 MALTTAARLLGKASCLVLAARHASASTNLKDLADLPKEQARIKTRQOHGKTVV 60
 OY 61 GOITVDMMYGGMRGKGLVETSVLPDEGIRFGFSIPECOKLLPKAKGGEPLPEGLF 120
 DB 61 GOITVDMMYGGMRGKGLVETSVLPDEGIRFGFSIPECOKLLPKAKGGEPLPEGLF 120
 OY 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
 DB 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
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 DB 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
 OY 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 DB 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 OY 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 DB 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 OY 241 TNLGTYDHOFTETLRILYLTITSHDEGGSVAHTSHLVGALSADPYLSFAAAMNGLAGPL 300
 DB 241 TNLGTYDHOFTETLRILYLTITSHDEGGSVAHTSHLVGALSADPYLSFAAAMNGLAGPL 300
 OY 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 DB 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 OY 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 DB 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 OY 361 REFALKHLRPNPMEFLVLAOLYKIVPNVLLLEGGKAKNPMPNDASHGVLLQYGTGMENY 420
 DB 361 REFALKHLRPNPMEFLVLAOLYKIVPNVLLLEGGKAKNPMPNDASHGVLLQYGTGMENY 420
 OY 421 TVLFVSRAAGVLAOLVMSRALGFLPRPKSMSTEGGLKPFVDSK 464
 DB 421 TVLFVSRAAGVLAOLVMSRALGFLPRPKSMSTEGGLKPFVDSK 464

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Testis;
 RX MEDLINE=21083660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsumoto Y., Nakai I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Holtmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seiya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kontuski S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC OXALACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 DR EMBL: AK005713; BAB24200.1; -
 DR HSSP: P00889; 2CTS.
 DR MGD: MGI:1919082; 1700007H16R1K.
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth.
 DR PRINTS: PR00143; CITRATESNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
 KW Lyase; Tricarboxylic acid cycle.
 SO SEQUENCE 466 AA; 52353 MW; 10A4746A109C491C CRC64;

Query Match 91.1%; Score 2219; DB 11; Length 466;
 Best Local Similarity 89.7%; Pred. No. 4.1e-172;
 Matches 418; Conservative 24; Mismatches 24; Indels 0; Gaps 0;

OY 1 MALTTAARLLGKASCLVLAARHASASTNLKDLADLPKEQARIKTRQOHGKTVV 60
 DB 1 MALTTAARLLGKASCLVLAARHASASTNLKDLADLPKEQARIKTRQOHGKTVV 60
 OY 61 GOITVDMMYGGMRGKGLVETSVLPDEGIRFGFSIPECOKLLPKAKGGEPLPEGLF 120
 DB 61 GOITVDMMYGGMRGKGLVETSVLPDEGIRFGFSIPECOKLLPKAKGGEPLPEGLF 120
 OY 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
 DB 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
 OY 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
 DB 121 WLVTGHTPTREQVSMLSKEMAKRAALPSSHVTMLDNPTNLHPMSQLSAAVTALNSSEN 180
 OY 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 DB 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 OY 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 DB 181 FARATAAGISIRTKRYEELIYEDSMDLAKLPVAAKTYRNKLRREGSGIGADISNDWSHNF 240
 OY 241 TNLGTYDHOFTETLRILYLTITSHDEGGSVAHTSHLVGALSADPYLSFAAAMNGLAGPL 300
 DB 241 TNLGTYDHOFTETLRILYLTITSHDEGGSVAHTSHLVGALSADPYLSFAAAMNGLAGPL 300
 OY 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 DB 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 OY 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 DB 301 HGLAQEVLVMTLOLQKEVGDVSEKLRDYIMNTLNSGRVVPVGGHVAVLKRTDPRYTCQ 360
 OY 361 REFALKHLRPNPMEFLVLAOLYKIVPNVLLLEGGKAKNPMPNDASHGVLLQYGTGMENY 420
 DB 361 REFALKHLRPNPMEFLVLAOLYKIVPNVLLLEGGKAKNPMPNDASHGVLLQYGTGMENY 420

QY 421 TVEGVSRALGVLAQIWSRALGEPLEPRKSMSTEGLMKFEVDSKSG 466
 Db 421 TVEGVSRALGVLSQIWSRALGEPLEPRKSMSTDLAKMEVNSERG 466

RESULT 5

09W401 PRELIMINARY; PRT; 464 AA.

AC 09W401;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-OCY-2002 (TEMBLrel. 22, Last annotation update)
 DE CG3861 protein (EC 4.1.3.7) (Citratesynthase).
 GN CG3861.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RX STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
 RA Butris J.C., Buschman D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Diets S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houch J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ijzerman C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclie J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen T.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC -1- OXALOACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 CC EMBL: A6003437; AAF46159.1; -;
 DR HSSP: P00889; 2CTS;
 DR FLYBase: FBgn0029869; CG3861.
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth. 1.
 DR PRINTS: PR00143; CITRATESYNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.

KW Lyase: Tricarboxylic acid cycle.
 SQ SEQUENCE 464 AA; 51574 MW; 57D582652931BAF9 CRC64;
 Query Match 71.3%; Score 1737.5; DB 5; Length 464;
 Best Local Similarity 70.5%; Pred. No. 6,7e-133;
 Matches 328; Conservative 50; Mismatches 80; Indels 7; Gaps 2;

QY 1 MALLTAARLLG---TKNASCLVLAARHNASSTNLKDLADLIRKQARIKTPYQOHG 56
 Db 1 MSLYRISARKLSBAQKLPNVGAYV---RMIAADGKSLRDVLAQVPOEGRVKNFRKHG 57

QY 57 KTYVGQITVMMGMRGMKGLYETNSVLDPPDGIIFRGSTTECKQLPKAKGSEPLP 116
 Db 58 ATKMGETTIDMMGMGMGKIKALVTERSVLDADGIRRGISTPECKQVPLAAGGTPELP 117

QY 117 EGFLLVLTGHIPTIEGVSWLSKEMAKRALPSSHVVTMLDNFTNHPNSQLSAAATYALN 176
 Db 118 EGFLLVLTGHIPTIEGVSWLSKEMAKRALPSSHVVTMLDNFTNHPNSQLSAAATYALN 177

QY 177 SESNFAVAAGISRTIKYWEIYEDSMDLAKLPVAAKIYRNLREGGSGIGAIIDSNDLW 236
 Db 178 HDSKFAKAYSDGVHKSKEYEVEDSMDLAKLPVVAATYCNTRYGKGSRISDSLDLW 237

QY 237 SHNFTNMLGTYDQFTETRLTYLTTHSDHGVSAHTSHLVSALSDEPTLSFAAMNGI 296
 Db 238 SANFVKNLGYDAPFELMLRYLTTHSDHGVSAHTSHLVSALSDEPTLSFAAMNGI 297

QY 297 ACPHLGLANQEVLMVLTQLOKEVGDVSDKRLDYTMNTLNSGVVPGYGAVALRKTDPR 356
 Db 298 ACPHLGLANQEVLMVLTQLOKEVGDVSDKRLDYTMNTLNSGVVPGYGAVALRKTDPR 357

QY 357 YTCQREFAKHLDPNDPMEKLVLAQIWSRALGEPLEPRKSMSTEGLMKFEVDSKSG 416
 Db 358 YTCQREFAKHLDPNDPMEKLVLAQIWSRALGEPLEPRKSMSTEGLMKFEVDSKSG 417

QY 417 MNYTYVFGVSRAIGVLAQIWSRALGEPLEPRKSMSTEGLMKFEVDSKSG 461
 Db 418 MNYTYVFGVSRAIGVLAQIWSRALGEPLEPRKSMSTEGLMKFEVDSKSG 462

RESULT 6

08T477 PRELIMINARY; PRT; 522 AA.

AC 08T477;
 DT 01-JUN-2002 (TEMBLrel. 21, Created)
 DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
 DE AT12538P (EC 4.1.3.7) (Citratesynthase) (CG3861-PB).
 GN CG3861.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RX SEQUENCE FROM N.A.
 RX Submittal (MAR-2002) to the EMBL/GenBank/DBJ databases.
 RA Ceiniker S.;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazet R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Butts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mettel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Mekhulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodruff M., Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*.";
 Science 287:2185-2195(2000).
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Ceiniker S.E., Adams M.D., Krommiller B., Man K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett E., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jaitani M., Kruse D., Li P., Mettel B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson K.A., Nuno J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirska R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RT "Sequencing of *Drosophila melanogaster* genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RN SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Ceiniker S.E.,
 RA Clamp M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of *Drosophila melanogaster* genome.";
 Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RN SEQUENCE FROM N.A.
 RA Adams M.D., Ceiniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.,
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RA FlyBase;
 CC Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC OXALACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 CC EMBL: AY089318; AAL90056.1; -
 DR EMBL: AE003437; AAN09169.1; -

DR FlyBase: FBgn0029869; CG3861.
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth. 1.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
 KM Lyase; tricarboxylic acid cycle.
 SQ SEQUENCE 522 AA; 58217 MW; 7CA9D79350F2764D CRC64;

Query Match 71.2%; Score 1735; DB 5; Length 522;
 Best Local Similarity 73.3%; Pred. NO. 1.3e-132;
 Matches 321; Conservative 48; Mismatches 69; Indels 0; Gaps 0;

QY 24 RHASASTNLKDLADLIPKQDARIKTFRQOHGKTVVGQITVDMYGGMRGKGLVETS 83
 Db 83 RMAADKSLRDVLAAPQEQDERVKRKHOGATKMGETITIDMYGMRGKGLVETS 142
 QY 84 VLDPDEGRFRFGFSIPKQKLLPRAKGEDELPKGLFVLLYTHGHPREDOYSLSKKAK 143
 Db 143 VLADDEGRFRFGFSIPKQKLLPRAKGEDELPKGLFVLLYTHGHPREDOYSLSKKAK 202
 QY 144 RAALPSHVYTMIDNEPTMLHPMSQLSAAVTAALNSESFARAAGISRTKYMEIYEDSM 203
 Db 203 RAALPQHVYTMIDNEPTMLHPMSQLSAAVTAALNDSKRAKYSQGVHKSKEYVEYEDSM 262
 QY 204 DLIAKLPVAAKIRYRNLREBSGIGALDSNLDWSHNTNMLGYTDHOFTELRLYLTHS 263
 Db 263 DLIAKLPVAAKIRYRNLREBSGIGALDSNLDWSHNTNMLGYTDHOFTELRLYLTHS 322
 QY 264 DHEGNGVSAHSHLYGSLSPDYLSFAAAMGGLGHLGLANOEVLMLOLOKEVGVCDV 323
 Db 323 DHEGNGVSAHSHLYGSLSPDYLSFAAAMGGLGHLGLANOEVLMLOLOKEVGVCDV 382
 QY 324 SDEKLDVYNTNLNSGRVVPYGVHAYLAKTDPRTYQREPAFLKHLPNPMKFLYAQLYKI 383
 Db 383 SEBOLKEVYNTNLNSGRVVPYGVHAYLAKTDPRTYQREPAFLKHLPNPMKFLYAQLYKI 442
 QY 384 VPNVLEGGKAKNPVNDASGVLLQYGTENMYTVLPGVSFALCVLAQLIWSRALG 443
 Db 443 VPPILTEGKAKNPVNDASGVLLQYGTENMYTVLPGVSFALCVLAQLIWSRALG 502
 QY 444 FPLRPKMSMEGIMKFPV 461
 Db 503 LPIERPSTFDLAKMV 520

RESULT 7
 ID 08NKF2 PRELIMINARY; PRT; 474 AA.
 AC 08NKF2;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Citrate synthase (EC 4.1.3.7).
 GN CITR.
 OS *Emmericella nidulans* (*Aspergillus nidulans*).
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 CC *Emmericella*; Trichocomaceae; *Emmericella*.
 OX NCBI_TaxID=162425;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA STRAIN-FGSC4;
 RC Seo S.W., Lee C.H., Maeng P.J.,
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC OXALACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 CC EMBL: AF468824; AAM22645.1; -
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth. 1.
 DR PRINTS: PR00143; CITRATESYNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
 KM Lyase; tricarboxylic acid cycle.
 SQ SEQUENCE 474 AA; 52160 MW; 879F9E95861ABDCF CRC64;

| RESULT 10 | | | |
|-----------------------|--|---------------------|-------------------|
| 09P688 | PRELIMINARY; | PRT; | 469 AA. |
| ID | 09P688 | | AC |
| AC | 09P688; | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, created) | | |
| DT | 01-OCT-2000 (TREMBLrel. 15, last sequence update) | | |
| DT | 01-OCT-2000 (TREMBLrel. 22, last annotation update) | | |
| DE | Mitochondrial citrate synthase (EC 4.1.3.7). | | |
| GN | BID1.330. | | |
| OS | Neurospora crassa. | | |
| OC | Eukaryotes; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | |
| OC | Sordariales; Sordariaceae; Neurospora. | | |
| OX | NCBI_Taxid=5141; | | |
| RN | (1) | | |
| RN | SEQUENCE FROM N.A. | | |
| RA | Schulte U., Algn V., Hohelsel J., Brandt P., Fartmann B., Holland R. | | |
| RA | Nyakatura G., Mewes H.W., Mannhaupt G.; | | |
| RL | Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. | | |
| RL | (2) | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | German Neurospora genome project; | | |
| RL | Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases. | | |
| CC | -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O + | | |
| CC | OXALOACETATE. | | |
| CC | -1- PATHWAY: TRICARBOXYLIC ACID CYCLE. | | |
| CC | -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY. | | |
| DR | EMBL: AL355927; CAB91282.1; " | | |
| DR | HSSP: P23007; 2CSC. | | |
| DR | InterPro: IPR002020; citrate_synth. | | |
| DR | Pfam: PF00285; citrate_synth. | | |
| DR | PRINTS: PR00143; CITRISYNTHASE. | | |
| DR | PROSITE: PS00480; CITRATE_SYNTHASE; 1. | | |
| KW | lysase; tricarboxylic acid cycle. | | |
| SO | SEQUENCE 469 AA; 51988 MW; C14FFDE07D345FD CRC64; | | |
| Query Match | 61.6%; | Score 1501.5; | DB 3; Length 469; |
| Best Local Similarity | 62.2%; | Pred. No. 1.le-113; | |

| | | | |
|----|-----|--|-----|
| Qy | 2 | ALLTAAARBLGTGRKNSCVLAAAHNASASTYIAKLIADLPKEQARIKTFRQOHTYVG | 61 |
| Db | 10 | AALRSSIHILTSQTA--FTARCVSSMTQTLKREFAELLPENIEKIKALKRKEHGSVVD | 66 |
| Qy | 62 | QITVDMMGGRMGKGLVETSVLDPDGIRFPGFSIPECOKLLPKAKGGEPLPGLEW | 121 |
| Db | 67 | KYTLDDVYGGAIGICLVWEGSVDPDAEGIRFRRKTIIPBECOLLPKAPGKEPLPDLFW | 126 |
| Qy | 122 | LVYTGHIIPEDBOVSMLSKEMAKRAALPHVVTMLDNPPTNLHPMSQSLAVTFLNLSNF | 181 |
| Db | 127 | LILTGVPSBEOQVROLSAEMAKRSVPKPIEBELLDRCPSDLIHPMAQSLATVLEHTSSF | 186 |
| Qy | 182 | ARAYAGISRTKYWMELIYEDSMDLIAKLPCVAAKIYRNLYREGSGIADSNLDWSHNF | 241 |
| Db | 187 | ARAYAGINKKEWGCYTFEDSMDLIAKLPTIARLYQVNF-GGKVAAYOKDDYSPFNA | 245 |
| Qy | 242 | NMLGTYDHO-FPELTRLYITITSHDEGGNSAHTSHLYGKSLSPYISFPAAMNGLAQL | 300 |
| Db | 246 | NOLGFEDNDPEELLRLYLTITHTDEGGNSAHTHTHLVGLSSPFLISVAAGNLGAPL | 305 |
| Qy | 301 | HGLANGEVLMVLTQLQEKYKDVSDSEKRDYINMTLNSGRVVPYCGHAVLRKTDPRYTCQ | 360 |
| Db | 306 | HGLANGEVLMVLTLEKKKVIIGDLSDEALTTKLTMLTIANGRVVPYCGHAVLRKTDPRKSNQ | 365 |
| Qy | 361 | REFALKHLPNDMPKFLVAQLYKIVPNVLLBEGAKKNPMPNVDAHSGVLLQYCGTENTNY | 420 |
| Db | 366 | RKFAOEHLPDEDPMLVLSQVYKIAKVLTEHGKTRKNPYPNVDAHSGVLLDHYGILTEANY | 425 |
| Qy | 421 | TVYFGSRALGVLAOLIMSRAALGPLREPKMSME | 455 |
| Db | 426 | TVLEGVSRALGVLPOLLIDRAVGAITERPCKSTSD | 460 |

[illegible]

Db 10 ATRAYSTAEPTLKERAEELLPGMOAEYKELSKHGKTVIGEVLLEQAYGCGMCIKGLWE 69
 QY 82 TSVLDEDEGIRFGFSIPECQKLLPRAKGEERLPBGLFWLVTGHIPTBEOYSWLSKEW 141
 Db 70 GSVLDEVEGIRFGKTIPTDIOKELPRAKESSEPLPEALFWLLLTGEVPTLAQTKAFAEL 129
 QY 142 AKRAALPSHYVTMLDNEPTNLHPMSQLSAAVNTALNSFSNPARAYAGCISTKTKWELIYED 201
 Db 130 ASSSALPKHVEDLDLDCPTLHPMAQFSLAINALEESKFAKAYAGVNNKEWKYKTED 189
 QY 202 SMDLKLPCVAAKIYRNLYREGSGIGAIINLDMWSHNFNTMLGYTDH-OFTETLTLYLT 260
 Db 190 SIDLLAKLPVAAKIRTNPKDKK-VAPVNASLDYSHNFANMLGFGDNKFEVLMRLYLS 248
 QY 261 IHSDEHGNSAHTSHLVGSLSDPYLSFAAAMNGLAGPLHGLANOEVLWLTQLOKEVG 320
 Db 249 IHSDEHGNSAHTSHLVGSLSDPYLSFAAAMNGLAGPLHGRANOEVLWLTQLOKEVG 308
 QY 321 KDY-SDEKLBDYIWNLTNSGRVYPGYGHAVLRTKTDPRYTQOREFALKHLPNDMPFKLYAQ 379
 Db 309 DDLFNEKEIEEYLMKTLNAGRVYGGHVALRKTDPYTAOREFALKHMPDYDMFKLVSN 368
 QY 380 LYKIVPNVLLDOCKANPNPNVDAHSGVLLQYGYGMEYNYTVLFGVSALAGVLAOLIMS 439
 Db 369 IYEVAPKVLAEQCKTNPNPNVDSHSGILLQYGYGMEYNYTVLFGVAPKAFVLPOLIID 428
 QY 440 RALGFPLERPKSMSTEGLMKEFVDS 463
 Db 429 RGLGMAIERPKSFSTOKYKELVEN 452

RESULT 12

ID 08SSP7 PRELIMINARY; PRT: 460 AA.
 AC 08SSP7;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2003 (TREMBLrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative lyase (EC 4.1.3.7) (Citrate synthase).
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_Taxid=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AX4;
 RA Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
 RA Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
 RA Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
 RT "Sequence and Analysis of Chromosome 2 of Dictyostelium."
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC OXALOACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 DR EMBL: AC116960; AAC08461.1; -
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth.1.
 DR PROSITE: PS00480; CITRATE_SYNTHASE.1.
 KM Lyase; Tricarboxylic acid cycle.
 SQ SEQUENCE 460 AA; 51220 MW; 1B4A0B58E4519E0 CRC64;

Query Match 60.9%; Score 1483.5; DB 5; Length 460;
 Best Local Similarity 61.7%; Pred. No. 3.2e-112;
 Matches 282; Conservative 66; Mismatches 104; Indels 5; Gaps 3;

QY 8 ARLLGTNRASCLVLAARHNASSTNLKDLADLPKQARIKTFRQOHGKTVVQGLVDM 67
 Db 3 ARLLGTNRASCLVLAARHNASSTNLKDLADLPKQARIKTFRQOHGKTVVQGLVDM 67
 QY 68 MYGGMKGLVETSVLDDEGIRFGFSIPECQKLLPRAKGEERLPBGLFWLVTGHI 127
 Db 59 AYCGMSVSKLWETSLDDEGIRFGKTIPTDIOKELPRAKESSEPLPEALFWLLLTGE 118

QY 128 IPTBEOYSWLSKEMAKRALPSHYVTMLDNEPTNLHPMSQLSAAVNTALNSFSNPARAYAG 187
 Db 119 VPTBEOYSWLSKEMAKRALPSHYVTMLDNEPTNLHPMSQLSAAVNTALNSFSNPARAYAG 178
 QY 188 GISRTYKWEIYDSMDLAKLPCVAAKIYRNLYREGSGIGAIINLDMWSHNFNTMLGYTDH 247
 Db 179 GYAKDKTWESTLSDSLDYLAKLPEVAALYQNTKKSDDITKIDENLDMWSANFNRLGTT 238
 QY 248 DHOETLTLYLTINSHDEHGNSAHTSHLVGSLSDPYLSFAAAMNGLAGPLHGLANOEVL 307
 Db 239 SKOFDELMLRYLTINSHDEHGNSAHTSHLVGSLSDPYLSFAAAMNGLAGPLHGLANOEVL 298
 QY 308 VLVWLTQLOKEVG-KYVSEKLDYIWNLTNSGRVYPGYGHAVLRTKTDPRYTQOREFALK 366
 Db 299 VLSMTKLOEKLCKNEVSEVSEALWEGINAGRVYGGHVALRKTDPYTAOREFALKHMPDY 358
 QY 367 HLPNDMPFKLYAQYKIVPNVLLDOCKANPNPNVDAHSGVLLQYGYGMEYNYTVLFGV 426
 Db 359 HLPNDMPFKLYAQYKIVPNVLLDOCKANPNPNVDAHSGVLLQYGYGMEYNYTVLFGV 418
 QY 427 SRALGVLAOLIMSRALGFPLERPKSMSTEGLMKEFVDS 463
 Db 419 SRAIGVLSLWMDRLIGHPIERPKSVTTEMISYILIS 455

RESULT 13

ID 09FUJ7 PRELIMINARY; PRT: 472 AA.
 AC 09FUJ7;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Citrate synthase (EC 4.1.3.7).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriophytidae; Oryzaeae; Oryza.
 OX NCBI_Taxid=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Silva da Silva A.L., Becker D., Loerz H.;
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: CITRATE + COA = ACETYL-COA + H(2)O +
 CC OXALOACETATE.
 CC -1- PATHWAY: TRICARBOXYLIC ACID CYCLE.
 CC -1- SIMILARITY: BELONGS TO THE CITRATE SYNTHASE FAMILY.
 DR EMBL: AF302906; AAC28777.1; -
 DR HSSP: P23007; 2CSC.
 DR Gramene: 09FUJ7; -
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth.1.
 DR PRINTS: PR00143; CITRATESYNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE.1.
 KM Lyase; Tricarboxylic acid cycle.
 SQ SEQUENCE 472 AA; 52228 MW; 52F7A2003FEF1811 CRC64;

Query Match 60.8%; Score 1481.5; DB 10; Length 472;
 Best Local Similarity 60.5%; Pred. No. 4.8e-112;
 Matches 277; Conservative 80; Mismatches 96; Indels 5; Gaps 3;

QY 4 LTAARILG--TKNASCL--VLAARHNASSTNLKDLADLPKQARIKTFRQOHGKTV 59
 Db 7 LTAARILG--TKNASCL--VLAARHNASSTNLKDLADLPKQARIKTFRQOHGKTV 59
 QY 60 VGOITVDMYMGKMGKGLVETSVLDDEGIRFGFSIPECQKLLPRAKGEERLPBGLFWLVTGHI 119
 Db 67 LGNITVDMYMGKMGKGLVETSVLDDEGIRFGFSIPECQKLLPRAKGEERLPBGLFWLVTGHI 126
 QY 120 FWLVTGHIPTBEOYSWLSKEMAKRALPSHYVTMLDNEPTNLHPMSQLSAAVNTALNSFS 179
 Db 127 FWLVTGHIPTBEOYSWLSKEMAKRALPSHYVTMLDNEPTNLHPMSQLSAAVNTALNSFS 186
 QY 180 NFARAYAGCISTKTKWELIYEDMDLAKLPCVAAKIYRNLYREGSGIGAIINLDMWSHNF 239

Db 317 EWLFLREEYKGDYKSETIETIMDTLNSGRVPGIGHAVLRKTDPRYTAOREFALKHP 376
QY 370 NDPMFKLVAAQLYKIVPNVLEOGKAKNPMPNVDAHSGVLLQYGYGTEMYTYVLFQVSR 429
Db 377 DYELFKLVSTIYEVAPGVLTGOGKTKNPMNPVNDHSGVLLQYGYGLTEASFYTVLFGV 436
QY 430 LGVLAQLMSRALGFPLERPKSMSTEGLMKFVDS 463
Db 437 FGVLPQLIIDRAVGOPIERPKSFSTEKEYIELVNS 470

Search completed: September 5, 2003, 20:10:48
Job time : 106 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2003, 20:02:47 : Search time 23 Seconds

(without alignments)
952,802 Million cell updates/sec

Title: US-09-996-223-1

Perfect score: 2436
Sequence: 1 MALLTAAARLLGTRNASCLV.....ERPKSMSTEGIAKFEVDSKSG 466

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|-------------|
| 1 | 2399 | 98.5 | 466 | 1 | CISY_HUMAN |
| 2 | 2339 | 96.0 | 464 | 1 | CISY_PIG |
| 3 | 2048 | 84.1 | 433 | 1 | CISY_CHICK |
| 4 | 1693 | 69.5 | 468 | 1 | CISY_CAEL |
| 5 | 1547.5 | 63.5 | 474 | 1 | CISY_EMENI |
| 6 | 1526.5 | 62.7 | 475 | 1 | CISY_ASPNG |
| 7 | 1519 | 62.4 | 473 | 1 | CISY_SCHPO |
| 8 | 1507.5 | 61.9 | 472 | 1 | CISY_SCHPO |
| 9 | 1501.5 | 61.6 | 469 | 1 | CISY_DAUCA |
| 10 | 1499.5 | 61.6 | 479 | 1 | CISY_NEUCR |
| 11 | 1498.5 | 61.5 | 473 | 1 | CISY_YEAST |
| 12 | 1442.5 | 59.2 | 467 | 1 | CISY_ARATH |
| 13 | 1435.5 | 58.9 | 471 | 1 | CISY_CANTR |
| 14 | 1425 | 58.5 | 460 | 1 | CISY_CITMA |
| 15 | 1385.5 | 56.9 | 469 | 1 | CISY_YEAST |
| 16 | 1349 | 55.4 | 471 | 1 | CISY_FRANR |
| 17 | 1219 | 50.0 | 462 | 1 | CISY_SOLTU |
| 18 | 1063.5 | 43.7 | 486 | 1 | CISY_TETTH |
| 19 | 356 | 14.6 | 437 | 1 | CISY_YEAST |
| 20 | 351 | 14.4 | 436 | 1 | CISY_CORGL |
| 21 | 346 | 14.2 | 437 | 1 | CISY_ACENC |
| 22 | 338 | 13.9 | 428 | 1 | CISY_SYNG3 |
| 23 | 332.5 | 13.6 | 431 | 1 | CISY_PSEAE |
| 24 | 331.5 | 13.6 | 411 | 1 | CISY_MYCTU |
| 25 | 328 | 13.5 | 411 | 1 | CISY_RICHA |
| 26 | 327.5 | 13.4 | 411 | 1 | CISY_RICHA |
| 27 | 327.5 | 13.4 | 411 | 1 | CISY_ASTRI |
| 28 | 327.5 | 13.4 | 430 | 1 | CISY_RICHA |
| 29 | 327.5 | 13.4 | 435 | 1 | CISY_RICHA |
| 30 | 325.5 | 13.4 | 411 | 1 | CISY_RICHA |
| 31 | 325.5 | 13.4 | 411 | 1 | CISY_RICHA |
| 32 | 325.5 | 13.4 | 411 | 1 | CISY_RICHA |
| 33 | 323.5 | 13.3 | 412 | 1 | CISY_RICHA |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 322.5 | 13.2 | 516 | 1 | CYSZ_CUCNA | P49299 cucurbita m |
| 35 | 319.5 | 13.1 | 411 | 1 | CISY_RICHA | O59732 rickettsia |
| 36 | 318.5 | 13.1 | 376 | 1 | CISY_PYRPU | O53554 pyrococcus |
| 37 | 317.5 | 13.0 | 411 | 1 | CISY_RICHA | O59748 rickettsia |
| 38 | 317.5 | 13.0 | 411 | 1 | CISY_RICHA | O59768 rickettsia |
| 39 | 315.5 | 13.0 | 427 | 1 | CISY_ECOLI | P00891 escherichia |
| 40 | 314.5 | 12.9 | 411 | 1 | CISY_RICHA | O59730 rickettsia |
| 41 | 314 | 12.9 | 423 | 1 | CISY_ACINA | P20902 acinetobact |
| 42 | 311.5 | 12.8 | 436 | 1 | CISY_RICPR | P09948 rickettsia |
| 43 | 307.5 | 12.6 | 431 | 1 | CISY_BAREE | P51033 bartonella |
| 44 | 306.5 | 12.6 | 427 | 1 | CISY_SALTY | O68883 salmonella |
| 45 | 305.5 | 12.5 | 411 | 1 | CISY_RICAU | P51039 rickettsia |

ALIGNMENTS

| RESULT 1 | ID | CISY_HUMAN | STANDARD: | PRT: | 466 AA. |
|----------|---|--------------------------------|-----------|-------------------------|---------|
| AC | O75390: | 15-JUL-1999 (Rel. 38, Created) | | | |
| DT | 15-JUL-1999 (Rel. 38, Last sequence update) | | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | | |
| DE | Citrate synthase, mitochondrial precursor (EC 2.3.3.1). | | | | |
| GN | CS. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Heart; | | | | |
| RX | MEDLINE=98026970; PubMed=9809442; | | | | |
| RA | Goldenhal M.J., Martin-Garcia J., Ananthakrishnan R.; | | | | |
| RT | "Cloning and molecular analysis of the human citrate synthase gene.;" | | | | |
| RL | Genome 41:733-738(1998). | | | | |
| CC | -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate -> citrate + COA. | | | | |
| CC | -1- PATHWAY: Tricarboxylic acid cycle. | | | | |
| CC | -1- SUBUNIT: Homodimer (by similarity). | | | | |
| CC | -1- SUBCELLULAR LOCATION: Mitochondrial matrix. | | | | |
| CC | -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS | | | | |
| CC | -1- CAPABLE OF OXIDATIVE METABOLISM. | | | | |
| CC | -1- SIMILARITY: Belongs to the citrate synthase family. | | | | |
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| CC | ----- | | | | |
| DR | EMBL: AF047042; AAC25560.1; - | | | | |
| DR | HSSP: P00889; 2CYS. | | | | |
| DR | GeneW: HGNC:2422; CS. | | | | |
| DR | GK: O75390; - | | | | |
| DR | MIM: 118950; - | | | | |
| DR | GO: GO:0005739; C:mitochondrion; TAS. | | | | |
| DR | GO: GO:0004108; F:citrate (SI)-synthase activity; TAS. | | | | |
| DR | InterPro: IPR002020; Citrate_synth. | | | | |
| DR | Pfam: PF00285; citrate_synth; 1. | | | | |
| DR | PRINTS: PR00143; CITRINASE. | | | | |
| DR | PROSITE: PS00480; CITRATE SYNTHASE; 1. | | | | |
| DR | TRANSFERRASE; Tricarboxylic acid cycle; Mitochondrion; Transit peptide. | | | | |
| FT | TRANSIT | 1 | 27 | | |
| FT | CHAIN | 28 | 466 | | |
| FT | ACT_SITE | 301 | 301 | | |
| FT | ACT_SITE | 347 | 347 | | |
| FT | ACT_SITE | 402 | 402 | | |
| FT | ACT_SITE | 402 | 402 | | |
| SO | SEQUENCE | 466 AA; | 51706 MW; | 878841484BD/CC80 CRC64; | |

Query Match 98.5%; Score 2399; DB 1; Length 466;
 Best Local Similarity 98.7%; Pred. No. 7.2e-173;
 Matches 460; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

1 MALTTAARLLGTRKNSCLVLAARHASASTNLKDILADLPKROARKTFEROHGKTVV 60
 1 MALTTAARLLGTRKNSCLVLAARHASASTNLKDILADLPKROARKTFEROHGKTVV 60
 61 GQITVDMVMYGMGMKGLVYETSVLPDEGIRFEGSIFPECCOKLLPRKNGEPLPGLE 120
 61 GQITVDMVMYGMGMKGLVYETSVLPDEGIRFEGSIFPECCOKLLPRKNGEPLPGLE 120
 121 WLVTGCIPTPEEYQSWLSKEMAKRALPSHYVTMLDNFPNLPMSQLSAAYVALNSES 180
 121 WLVTGCIPTPEEYQSWLSKEMAKRALPSHYVTMLDNFPNLPMSQLSAAYVALNSES 180
 181 FARAYAGISRTKRWELIYEDSMDLAKPCVAAKIYRNLYREGSGIGALDSNIDMSHNF 240
 181 FARAYAGISRTKRWELIYEDSMDLAKPCVAAKIYRNLYREGSGIGALDSNIDMSHNF 240
 241 TNNLGYTDHOFTELTRLTYLTIHSDHEGNAVSAHTSHLVGSALSDPYLSFAAAMGLAGPL 300
 241 TNNLGYTDHOFTELTRLTYLTIHSDHEGNAVSAHTSHLVGSALSDPYLSFAAAMGLAGPL 300
 301 HGLANQEVLYWLOLOKEVQKDVSDKLRDIYINNTLNSGRVPGYGYAVLRKTDPRYTCQ 360
 301 HGLANQEVLYWLOLOKEVQKDVSDKLRDIYINNTLNSGRVPGYGYAVLRKTDPRYTCQ 360
 361 REFALKHLPNDDPMFKLVAQLKXIVPNVLLBQGRKAKNPVNDASGVLLQYGGTEENNY 420
 361 REFALKHLPNDDPMFKLVAQLKXIVPNVLLBQGRKAKNPVNDASGVLLQYGGTEENNY 420
 421 TVLFGVSALGVLAQLIWSRALGFLPERKSMSTEGIMKTVDSKSG 466
 421 TVLFGVSALGVLAQLIWSRALGFLPERKSMSTEGIMKTVDSKSG 466

RESULT 2
 CIST_PIG ID CIST_PIG STANDARD; PRT; 464 AA.
 AC P00889;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Citrate synthase, mitochondrial precursor (EC 2.3.3.1).
 GN CS.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID-9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-89000665; PubMed-3048387;
 RA Evans C.T., Owens D.D., Sumegi B., Kispal G., Sreere P.A.;
 RT "Isolation, nucleotide sequence, and expression of a cDNA encoding
 RT pig citrate synthase".
 RL Biochemistry 27:4680-4686(1988).
 RN [2]
 RP SEQUENCE OF 28-464.
 RX MEDLINE-82231993; PubMed-7093227;
 RA Bloxham D.P., Parmelee D.C., Kumar S., Walsh K.A., Titani K.;
 RT "Complete amino acid sequence of porcine heart citrate synthase".
 RL Biochemistry 21:2028-2036(1982).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 AND 1.7 ANGSTROMS).
 RX MEDLINE-83010291; PubMed-7120407;
 RA Remington S., Wiegand G., Huber R.;
 RT "Crystallographic refinement and atomic models of two different forms
 RT of citrate synthase at 2.7- and 1.7-A resolution".
 RL J. Mol. Biol. 158:111-132(1982).
 RN [4]
 RP MUTAGENESIS.
 RX MEDLINE-91104711; PubMed-1702991;

RA Alter G.M., Casazza J.P., Zhi W., Nemeth P., Sreere P.A., Evans C.T.;
 RT "Mutation of essential catalytic residues in pig citrate synthase.";
 RL Biochemistry 29:7557-7563(1990).
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
 COA.
 CC -1- PATHWAY: Tricarboxylic acid cycle.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CC CAPABLE OF OXIDATIVE METABOLISM.
 CC -1- SIMILARITY: Belongs to the citrate synthase family.
 CC
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 CC
 CC
 CC EMBL; M21197; AAA31017.1; -.
 DR PIR; A29966; YKPG.
 DR PDB; 1CTS; 16-JUL-88.
 DR PDB; 2CTS; 09-OCT-88.
 DR PDB; 3CTS; 09-OCT-88.
 DR PDB; 4CTS; 16-JUL-88.
 DR InterPro; IPR002020; Citrate_synth.
 DR Pfam; PF00285; citrate_synth; 1.
 DR PRINTS; PR00143; CITRATESYNTHASE.
 DR PROSITE; PS00480; CITRATE SYNTHASE; 1.
 DR Transferrase; Tricarboxylic acid cycle; Mitochondrion; 3D-structure;
 KW Transist peptide; Methylation.
 KM
 FT TRANSIT 1
 FT CHAIN 28 464
 FT MOD_RES 395 395
 FT ACT_SITE 301 301
 FT ACT_SITE 347 347
 FT ACT_SITE 402 402
 FT ACT_SITE 402 402
 FT HELIX 33 55
 FT HELIX 56 57
 FT HELIX 57 57
 FT HELIX 65 69
 FT HELIX 70 71
 FT TURN 73 74
 FT STRAND 84 86
 FT STRAND 87 89
 FT STRAND 90 92
 FT STRAND 97 97
 FT HELIX 98 104
 FT STRAND 107 107
 FT STRAND 114 114
 FT HELIX 116 125
 FT HELIX 131 143
 FT TURN 144 144
 FT HELIX 149 157
 FT HELIX 164 174
 FT HELIX 175 178
 FT HELIX 180 186
 FT TURN 187 188
 FT TURN 191 193
 FT HELIX 194 221
 FT TURN 223 224
 FT TURN 232 233
 FT HELIX 236 244
 FT TURN 245 245
 FT HELIX 249 261
 FT TURN 262 262
 FT TURN 266 268
 FT HELIX 270 279
 FT TURN 280 282
 FT HELIX 285 296
 FT TURN 297 297
 FT TURN 299 303
 FT HELIX 304 318


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FT TURN 218 218
FT HELIX 222 234
FT TURN 235 235
FT HELIX 243 252
FT TURN 253 255
FT HELIX 258 269
FT TURN 270 270
FT TURN 272 276
FT HELIX 277 291
FT TURN 292 293
FT HELIX 298 310
FT TURN 311 312
FT STRAND 316 317
FT HELIX 318 318
FT HELIX 328 340
FT TURN 342 343
FT HELIX 345 364
FT TURN 365 365
FT STRAND 372 372
FT TURN 374 374
FT HELIX 375 384
FT TURN 385 386
FT HELIX 390 392
FT HELIX 393 414
FT TURN 415 416
FT HELIX 427 433
SQ SEQUENCE 433 AA; 47373 MM; 6942294BA95A9E06 CRC64;

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Query Match 84.1%; Score 2048; DB 1; Length 433;
Best Local Similarity 90.5%; Pred. No. 1.6e-146;
Matches 390; Conservative 10; Mismatches 31; Indels 0; Gaps 0;

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QY 28 ASSTNKLADIADLPEQARIKTFROOHGKTVVGQITVDMYGMGMKGLVETSYLDP 87
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 ASSTNKLADYLAALPEQARIKTFROOHGKTALGOITVDMSYGMGMKGLVETSYLDP 60
QY 88 DEGIRRGFSIPRCOKLLPRKAGGEPLREGLFMLVTGHIIPTEEOYSMLSKEMAKRAAL 147
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 DEGIRRGFSIPRCOKLLPRKAGGEPLREGLFMLVTGHIIPTEEOYSMLSKEMAKRAAL 120
QY 148 PSHVVTMLDNFTNLPMSQLSAAYVALNSSENFARAAYAGISRTXYWELIYEDSMOLA 207
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 PSHVVTMLDNFTNLPMSQLSAAYVALNSSENFARAAYAGISRTXYWELIYEDSMOLA 180
QY 208 KLPVAAKIYRNLYREGSGIGATDSNDSNFTNMLGYTDHOFTELTRYLYTIHSHDEG 267
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 KLPVAAKIYRNLYREGSGIGATDSNDSNFTNMLGYTDHOFTELTRYLYTIHSHDEG 240
QY 268 GNVSAHTSHLVGALSADPYLSFAAAMNGLAGPLHGLANOEVLMLOLQAXXAGADAS 327
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 GNVSAHTSHLVGALSADPYLSFAAAMNGLAGPLHGLANOEVLMLOLQAXXAGADAS 300
QY 328 LRDIYWNLTNSGRVVEGYGHAVALRKTDPRTYTCQREFALKHLPNDPMFKLVLAOLYKIVPNV 387
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 LRDIYWNLTNSGRVVEGYGHAVALRKTDPRTYTCQREFALKHLPNDPMFKLVLAOLYKIVPNV 360
QY 388 LLEOGAKKMPWPNVDHSGVLLQYGTENNTYTVLFVSRALGVLAQLIWSRSLGPPLE 447
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 361 LLEOGAKKMPWPNVDHSGVLLQYGTENNTYTVLFVSRALGVLAQLIWSRSLGPPLE 420
QY 448 RPKSMSTEGLM 458
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 421 RPKSMSTEGLM 431

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RESULT 4
CISY_CAEEL STANDARD; PRT; 468 AA.

AC P34575;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Probable citrate synthase, mitochondrial precursor (EC 2.3.3.1).

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GN T20G5.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxId=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISCOL N2;
RA Berkis M., Smith A.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
CC COA.
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -1- SIMILARITY: Belongs to the citrate synthase family.
CC -----
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CC -----
DR EMBL; Z30423; CAAB3004.1; -.
DR PIR; S42370; S42370.
DR HSSP; P23007; 2CSC.
DR WormRep; T20G5.2; CE00513.
DR InterPro; IPR002020; Citrate-synt.
DR Pfam; PF00285; Citrate-synt; 1.
DR PRINTS; PR00143; CITRATSYNTHASE.
DR PROSITE; PS00480; CITRATE SYNTHASE; 1.
KM Hypothetical protein; Transferase; Tricarboxylic acid cycle;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 2
FT CHAIN ? 468 MITOCHONDRION (POTENTIAL).
FT ACT_SITE 303 303 PROBABLE CITRATE SYNTHASE.
FT ACT_SITE 349 349 BY SIMILARITY.
FT ACT_SITE 404 404 BY SIMILARITY.
SQ SEQUENCE 468 AA; 51540 MM; CDE40CCA5729B9BEA CRC64;

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Query Match 69.5%; Score 1693; DB 1; Length 468;
Best Local Similarity 68.3%; Pred. No. 8.3e-120;
Matches 315; Conservative 62; Mismatches 82; Indels 2; Gaps 1;

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QY 1 MALTTAARLLGFKNA--SCLVLAARHASSTNKLADIADLPEQARIKTFROOHGKT 58
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MSLSGMAIRRLITKGYIPVCQVAPLSTSAEGSTNLEEVASKLIPAHNAKYKSRTEHGSI 60
QY 59 VGOQITVDMMYGMGMKGLVETSYLDPDEGIRRGFSIPRCOKLLPRKAGGEPLREG 118
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 VGOQITVDMMYGMGMKGLVETSYLDPDEGIRRGFSIPRCOKLLPRKAGGEPLREG 120
QY 119 LFWLVTGHIPTTEOYSMLSKEMAKRAALPSHYVTMLDNFTNLPMSQLSAAYVALNS 178
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 LFWLVTGHIPTTEOYSMLSKEMAKRAALPSHYVTMLDNFTNLPMSQLSAAYVALNS 180
QY 179 SNFARAAYAGISRTXYWELIYEDSMOLALPCVAAKIYRNLYREGSGIGATDSNDSN 238
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 181 SNFARAAYAGISRTXYWELIYEDSMOLALPCVAAKIYRNLYREGSGIGATDSNDSN 240
QY 239 NPTNMLGYTDHOFTELTRYLYTIHSHDEGNSAHTSHLVGALSADPYLSFAAAMNGLAG 298
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 241 NPTNMLGYTDHOFTELTRYLYTIHSHDEGNSAHTSHLVGALSADPYLSFAAAMNGLAG 300
QY 299 PLHGLANOEVLMLOLQAXXAGADASDEKLVDYIMNTLSGRVVEGYGHAVALRKTDPRT 358
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 301 PLHGLANOEVLMLOLQAXXAGADASDEKLVDYIMNTLSGRVVEGYGHAVALRKTDPRT 360
QY 359 COREFALKHLPNDPMFKLVLAOLYKIVPNVLLLEOGAKKMPWPNVDHSGVLLQYGTENN 418

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DB 361 COREEALKHLPPNDLJFKLVSTLYKTPGILLEGQAKAKNPVNDHSHGVLLQYFGMTKMS 420
OY 419 YTVLFGVSRALGVLAOLIMSRALGFLERPKSMSTEGLMK 459
DB 421 FTVLFGVSRALGVLSOLIMWARGMLERPKSHSTDGLK 461

RESULT 5
CISY_EMENT
ID CISY_EMENT STANDARD: PRT: 474 AA.
AC 000098;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Citrate synthase, mitochondrial precursor (EC 2.3.3.1).
GN CITR.
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FGSC 4;
RC MEDLINE=97306446; PubMed=9163747;
RA Park B.W., Han K.H., Lee C.Y., Lee C.H., Maeng P.J.;
RT "Cloning and characterization of the citA gene encoding the
RT mitochondrial citrate synthase of Aspergillus nidulans."
RL Mol. Cells 7:290-295(1997).
CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate -> citrate +
CC CoA.
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -1- SIMILARITY: Belongs to the citrate synthase family.
CC -----
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CC -----
DR EMBL: U89675; AAC49728.1; -
DR HSSP: P23007; 2CSC.
DR InterPro: IPR002020; Citrate_synth.
DR Pfam: PF00285; citrate_synth; 1.
DR PRINTS: PRO0143; CITRSTNTASE.
DR PROSITE: PS00480; CITRATE SYNTHASE: 1.
KM Transferase: Tricarboxylic acid cycle; Mitochondrion; Transit peptide.
FT TRANSIT 1 35
FT CHAIN 36 474
FT ACT_SITE 310 310 CITRATE SYNTHASE.
FT ACT_SITE 356 356 BY SIMILARITY.
FT ACT_SITE 411 411 BY SIMILARITY.
FT ACT_SITE 411 411 BY SIMILARITY.
SO SEQUENCE 474 AA: 52223 MW; E2E86892ACB5398B CRC64;

Query Match 63.5%; Score 1547.5; DB 1; Length 474;
Best Local Similarity 62.2%; Pred. No. 7.3e-109;
Matches 294; Conservative 68; Mismatches 96; Indels 15; Gaps 3;
OY 6 AAARLGTKNASCLVLAAR-----HASASSTNLKDIADLIPKQARIKTFR 52
DB 2 ASTLRLSTLSALRSSTLAAKPVQVAENGLRCYSTGKTSIKETRADKLGLGELEVKKLR 61
OY 53 QOHGKTVVGOITVDMYGGMRGKGLVETVLDPEDEGIRFGFSIPECOKLLPRAKGE 112
DB 62 KEHGKVIYGEILLDQAYGARGVKCLVWGSVLDESEGRFRGGLTIPKQKLLPRAKGE 121
OY 113 EPLPGGLWLVLTGHIIPTEBOYSWLSKEMAKRALPSHVYMLDNEPTNLHPMSQLSAAV 172

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DB 122 EPLPGGLWLVLTGVEPSEQVDLSAEMARSDLPKFIIEIDLRYVSTLHPMAQFSLAV 181
OY 173 TALNSESNFARAAYAGISRTKRWELIERSMDLAKLPVAKIYRNLYREGSGIGAIDS 232
DB 182 TALEHESAPAKATKATKINKKDWNTYFEDSMDLAKLPYIAKIRRWKDKR-VAPIOK 240
OY 233 NIDWSHNFTNMLGYTDHQ-FTELTRLYLTIRHSDHEGANSVHTSHLYGSALSDPYLSFNA 291
DB 241 DKDYSNLANOJGFPADNKFVELMLRXYLTIRHSDHEGANSVHTSHLYGSALSDPYLSFNA 300
OY 292 ANGLAGPLHGLANDVWLTLQLOKENGKDVSDKLRDYINNTLNSGRVPGYGHAVLR 351
DB 301 GLNGLAGPLHGLANDVWLTLQLOKENGKDVSDKLRDYINNTLNSGRVPGYGHAVLR 360
OY 352 KTDPRYTQOREFALKHLPPNDLJFKLVSTLYKTPGILLEGQAKAKNPVNDHSHGVLLQY 411
DB 361 KTDPRYTQOREFALKHLPPNDLJFKLVSTLYKTPGILLEGQAKAKNPVNDHSHGVLLQY 420
OY 412 YGMTENMYTVLFGVSRALGVLAOLIMSRALGFLERPKSMSTEGLMKFPVDSK 464
DB 421 YGLTERNYTVLFGVSRALGVLPOLLIDRAFAPLERPKSFSTENYAKLVGAK 473

RESULT 6
CISY_ASPIRG
ID CISY_ASPIRG STANDARD: PRT: 475 AA.
AC P51044;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Citrate synthase, mitochondrial precursor (EC 2.3.3.1).
GN CIT-1.
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_TaxID=5061;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WU-2223L;
RA Oshida Y., Miyake K., Kanayama S., Kitamura K., Usami S.;
RT Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
RL -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate -> citrate +
CC CoA.
CC -1- PATHWAY: Tricarboxylic acid cycle.
CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix (By similarity).
CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
CC CAPABLE OF OXIDATIVE METABOLISM.
CC -1- SIMILARITY: Belongs to the citrate synthase family.
CC -----
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CC -----
DR EMBL: D63376; BA009691.1; -
DR HSSP: P23007; 2CSC.
DR InterPro: IPR002020; Citrate_synth.
DR Pfam: PF00285; citrate_synth; 1.
DR PRINTS: PRO0143; CITRSTNTASE.
DR PROSITE: PS00480; CITRATE SYNTHASE: 1.
KM Transferase: Tricarboxylic acid cycle; Mitochondrion; Transit peptide.
FT TRANSIT 1 475
FT CHAIN 475 475
FT ACT_SITE 310 310 CITRATE SYNTHASE.
FT ACT_SITE 356 356 BY SIMILARITY.
FT ACT_SITE 411 411 BY SIMILARITY.
FT ACT_SITE 411 411 BY SIMILARITY.
SO SEQUENCE 475 AA: 52153 MW; F93525B3F1FCB3F CRC64;

Query Match 62.7%; Score 1526.5; DB 1; Length 475;
Best Local Similarity 62.5%; Pred. No. 2.8e-107;

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Db 426 QSEYTVLFGVSRFLGVASQLIMDRALGLPIERPKSFSTALKKWEK 473

RESULT 8

| ID | CISY_DAUCA | STANDARD: | PRT: | 472 AA. |
|----|--|-----------|------|---------|
| AC | 080433; | | | |
| DT | 16-OCT-2001 (Rel. 40, Created) | | | |
| DT | 16-OCT-2001 (Rel. 40, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Citrate synthase, mitochondrial precursor (EC 2.3.3.1). | | | |
| GN | CS. | | | |
| OS | Daucus carota (Carrot). | | | |
| OC | Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | |
| OC | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; | | | |
| OC | Asteridae; campanulids; Apiales; Apiaceae; Daucus. | | | |
| OX | NCBI_TaxID=4039; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=cv. MS Yonson; | | | |
| RA | Takita E., Koyama H., Shitano Y., Shibata D., Hara T.; | | | |
| RT | "cDNA encoding carrot mitochondrial citrate synthase." | | | |
| RL | Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases. | | | |
| CC | -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate + CoA. | | | |
| CC | -1- PATHWAY: Tricarboxylic acid cycle. | | | |
| CC | -1- SUBUNIT: Homodimer (By similarity). | | | |
| CC | -1- SUBCELLULAR LOCATION: Mitochondrial matrix. | | | |
| CC | -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM. | | | |
| CC | -1- SIMILARITY: Belongs to the citrate synthase family. | | | |
| CC | ----- | | | |
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| CC | ----- | | | |
| DR | EMBL: AB017159; BAA32557.1; - | | | |
| DR | HSSP: P23007; 2CSC | | | |
| DR | InterPro: IPR002020; Citrate_synth. | | | |
| DR | PIfam: Pf00285; citrate_synth.1. | | | |
| DR | PRINTS: PR00143; CITRATESYNTHASE. | | | |
| DR | PROSITE: PS00480; CITRATE SYNTHASE. 1. | | | |
| KW | Transferrase; Tricarboxylic acid cycle; Mitochondrion; Transit peptide. | | | |
| FT | TRANSIT 1 ? MITOCHONDRION (POTENTIAL). | | | |
| FT | CHAIN ? 472 CITRATE SYNTHASE. | | | |
| FT | ACT_SITE 308 308 BY SIMILARITY. | | | |
| FT | ACT_SITE 354 354 BY SIMILARITY. | | | |
| FT | ACT_SITE 409 409 BY SIMILARITY. | | | |
| SO | SEQUENCE 472 AA; 52656 MW; A6C8CFCAL7142120 CnC64; | | | |

Query Match 61.9%; Score 1507.5; DB 1; Length 472;
 Best Local Similarity 64.7%; Pred. No. 7.3e-106;
 Matches 279; Conservative 60; Mismatches 91; Indels 1; Gaps 1;

Db 426 QSEYTVLFGVSRFLGVASQLIMDRALGLPIERPKSFSTALKKWEK 473

RESULT 9

| ID | CISY_NEUCR | STANDARD: | PRT: | 469 AA. |
|----|--|-----------|------|---------|
| AC | P34085; O9P688; | | | |
| DT | 01-FEB-1994 (Rel. 28, Created) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last sequence update) | | | |
| DT | 15-SEP-2003 (Rel. 42, Last annotation update) | | | |
| DE | Citrate synthase, mitochondrial precursor (EC 2.3.3.1). | | | |
| GN | Cit-1 OR Bld1.330. | | | |
| OS | Neurospora crassa. | | | |
| OC | Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; | | | |
| OC | Sordariomycetidae; Sordariales; Sordariaceae; Neurospora. | | | |
| OX | NCBI_TaxID=5141; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=74A; | | | |
| RX | MEDLINE=94104594; PubMed=7904043; | | | |
| RA | Retea T., Contreas E.T., Ong T., Bowman E.J., Bowman B.J.; | | | |
| RT | "Characterization of the cit-1 gene from Neurospora crassa encoding the mitochondrial form of citrate synthase." | | | |
| RL | Mol. Gen. Genet. 242:105-110(1994). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=74A-OR23-1A / FGSC 987; | | | |
| RX | PubMed=12655011; | | | |
| RA | Mannhaupt G., Montione C., Haase D., Mewes H.-W., Aign V., | | | |
| RA | Hohnleisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J., | | | |
| RT | Schulte U.; | | | |
| RT | "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence." | | | |
| RL | Nucleic Acids Res. 31:1944-1954(2003). | | | |
| CC | -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate + CoA. | | | |
| CC | -1- PATHWAY: Tricarboxylic acid cycle. | | | |
| CC | -1- SUBCELLULAR LOCATION: Mitochondrial matrix. | | | |
| CC | -1- DEVELOPMENTAL STAGE: ABUNDANT AFTER 6-12 HRS OF GROWTH. IT IS NOT SIGNIFICANTLY EXPRESSED AFTER 24 HRS, WHICH IS SEVERAL HRS AFTER ENTERING THE STATIONARY PHASE OF GROWTH. | | | |
| CC | -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM. | | | |
| CC | -1- SIMILARITY: Belongs to the citrate synthase family. | | | |
| CC | ----- | | | |
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| CC | ----- | | | |
| DR | EMBL: M84187; AAA16630.1; - | | | |
| DR | EMBL: AL355927; CAB91282.1; - | | | |
| DR | PIR: S41563; S41563. | | | |
| DR | HSSP: P23007; 2CSC. | | | |
| DR | InterPro: IPR002020; Citrate_synth. | | | |

Query Match 61.9%; Score 1507.5; DB 1; Length 472;
 Best Local Similarity 64.7%; Pred. No. 7.3e-106;
 Matches 279; Conservative 60; Mismatches 91; Indels 1; Gaps 1;

DR pfam: PF00285; citrate_synth. 1.
 DR PRINTS: PR00143; CITRATESYNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE. 1.
 KW Tricarboxylic acid cycle; Mitochondrion; Transit peptide;
 MW Multigene family.
 FT TRANSIT 1 33 MITOCHONDRION (POTENTIAL).
 FT CHAIN 34 469 CITRATE SYNTHASE.
 FT ACT_SITE 352 352 BY SIMILARITY.
 FT CONFLICT 351 351 G -> A (IN REF. 1).
 SQ SEQUENCE 469 AA; 51988 MW; C14PFDE07D345FD CRC64;

Query Match 61.6%; Score 1501.5; DB 1; Length 469;
 Best Local Similarity 62.2%; Pred. No. 2.1e-105;
 Matches 283; Conservative 79; Mismatches 88; Indels 5; Gaps 3;

QY 2 ALTTAAARLLGTKNASCLVLAARHAGASSTNLKDLADLPKQARIKTFROQHGKTVG 61
 DB 10 AALRSSIHLSRQTA--FTAAACYSSTKQTLKERRAFELLPEIKIKLRKHSKYVD 66
 QY 62 QITVDMMGGMGMKGLVETSVLPDEGIRFGESIPFCQKLLPRAKGGEPLPGLFM 121
 DB 67 KYLLDDVYGARGIKCLVWEGSVLDAEEGIRFGKTIPEQQLLPKAPGGEPLPGLFM 126
 QY 122 LVTYGHIPTEEOVWMLSKEMAKRALPSHYVTMLDNFPPTLHPMSQLSAVTAALNSESNF 181
 DB 127 LLITGEVPEEQVROLSAEHARSVDYKTEELIDKCPDLHPMAQLSTAVTALEHTSSF 186
 QY 182 ARAAGISRTKYMELIYEDSMDLAKLPCVAAKIYRNLYREGSGIGALDSNLDMSHNFT 241
 DB 187 ARAYAGINKKEWGTPEDSMDLAKLPTIARIYQNVFK-GGVAAVQKMDYFNF 245
 QY 242 NMIGTYDHO-FTTILTYLYTHSDHEGCVSAHTSHLSVGSALDPLTSFAAMNGIACPL 300
 DB 246 NDLGFDNDVEFLLYLTHIDHEGCVSAHTSHLSVGSALSPFLSVAAAGLNGIACPL 305
 QY 301 HGLANQEVLMWLTQLKEVGDVSDKLRDYINNTLNSGVVYGYGHAUVRKTDPRYTCO 360
 DB 306 HGLANQEVLMWLTQLKEVGDVSDKLRDYINNTLNSGVVYGYGHAUVRKTDPRYTCO 365
 QY 361 REFALKHLPNDPFEKLVQALYKIVPNVLEQGRKAKNPWNVDAHSGVLLQYGMTEMY 420
 DB 366 RKAQHLRDEDPFQVLSQYVKAIVLTHGKTKNPYPNVDAHSGVLLQYGLTANY 425
 QY 421 TVLFGSRALGVLAQLINSRACGLPERKSKMSTE 455
 DB 426 TVLFGSRALGVLPOLLIDRAVGAPLERKSYSTD 460

RESULT 10
 CITSY_YEAST STANDARD: PRT; 479 AA.

AC P00890;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-FEB-1994 (Rel. 28, last sequence update)
 DT 15-SEP-2003 (Rel. 42, last annotation update)
 DE citrate synthase, mitochondrial precursor (EC 2.3.3.1).
 GN CIT1 OR LIFS OR GLU3 OR YNR001C OR N2019.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=D273-10B;
 RA Linder P., Blueckthun A.;
 RL Submitted (JUL-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D273-10B;
 RX MEDLINE=85003587; PubMed=6090126;
 RA Suisa M., Suda K., Schatz G.;
 RT "Isolation of the nuclear yeast genes for citrate synthase and
 fifteen other mitochondrial proteins by a new screening method.";

RL EMBO J. 3:1773-1781(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=5288C / FY1679;
 RX MEDLINE=95208356; PubMed=7900425;
 RA Verhasselt P., Aert R., Voet M., Volckaert G.;
 RT "Twelve open reading frames revealed in the 23.6 kb segment flanking
 the centromere on the Saccharomyces cerevisiae chromosome XIV right.
 RT arm.";
 RT yeast 10:1355-1361(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GRF88;
 RX MEDLINE=95028151; PubMed=7941739;
 RA Lalo D., Stettler S., Mariotte S., Gendreau E., Thuriaux P.;
 RT "Organization of the centromeric region of chromosome XIV in
 Saccharomyces cerevisiae.";
 RL yeast 10:523-533(1994).
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate +
 COA.
 CC -1- PATHWAY: Tricarboxylic acid cycle.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CAPABLE OF OXIDATIVE METABOLISM.
 CC -1- SIMILARITY: Belongs to the citrate synthase family.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: 223259; CAA80781.1; -
 DR EMBL: X00782; CAA25359.1; -
 DR EMBL: X77395; CAA54569.1; -
 DR EMBL: Z71616; CAA96277.1; -
 DR PIR: S35390; YKBY.
 DR HSSP: P23007; 2CSC.
 DR SGD: S0005284; CIT1.
 DR GO: GO:0005739; C:mitochondrion; IDA.
 DR InterPro: IPR002020; Citrate_synth.
 DR pfam: PF00285; citrate_synth. 1.
 DR PRINTS: PR00143; CITRATESYNTHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE. 1.
 KW Tricarboxylic acid cycle; Mitochondrion; Transit peptide;
 MW Multigene family.
 FT TRANSIT 1 37 MITOCHONDRION.
 FT CHAIN 38 479 CITRATE SYNTHASE.
 FT ACT_SITE 312 312 BY SIMILARITY.
 FT ACT_SITE 358 358 BY SIMILARITY.
 FT ACT_SITE 413 413 BY SIMILARITY.
 FT CONFLICT 58 58 E -> Q (IN REF. 2).
 FT CONFLICT 78 78 E -> EE (IN REF. 2).
 SQ SEQUENCE 479 AA; 53360 MW; 280661B1CB248F14 CRC64;

Query Match 61.6%; Score 1499.5; DB 1; Length 479;
 Best Local Similarity 62.2%; Pred. No. 3e-105;
 Matches 280; Conservative 76; Mismatches 89; Indels 5; Gaps 3;

QY 20 VLAARH-ASASSTNLKDILLADLPKQARIKTFROQHGKTVGQITVDMMGGMKGL 78
 DB 31 LNAARHSSASDEQTLKERRAFELLPAKAEIKRKKGKTVIGEVLLQVAGMKGKGL 90
 QY 79 VVETSVLPDEGIRFGESIPFCQKLLPRAKGGEPLPGLFWLVTGHIPTDEQVSWLS 138
 DB 91 VMEGSVLPDEGIRFGESIPFCQKLLPRAKGGEPLPGLFWLVTGHIPTDAQVKALS 150
 QY 139 KEWAKRALPSHYVTMLDNFPPTLHPMSQLSAVTAALNSESNFARAAGISRTKYWELI 198
 DB 151 ADLAARSEIPEHVITQLDLSLPKDLHPMAQLSTAVTALESESKFAKAYAGVSKKEYWSTY 210

QY 199 YEDSMDLIAKPCVAARIYRLYREGSGIGAIDSNLDMNSHFTNMLGYTDHOFTETRLY 258
 DB 211 FEDSLDLKLPVIAASKIYRNVFKGK - ITSTDPRADYCGKMLAQGLKENDDFIDMLRLY 269
 QY 259 LTHSDHGGVNSAHTSHLVGSALSDPYLSFAAAMNGIAGPLHGLANOEVWLTOLOKE 318
 DB 270 LTHSDHGGVNSAHTSHLVGSALSDPYLSFAAAMNGIAGPLHGLANOEVWLTOLOKE 329
 QY 319 VGRVSDPKLDYDWTNLTNSGRVVGXGAVLRTDPRYTCDDREFALHLPNDPMEKLYA 378
 DB 330 VKGYSKETIKYIMDLTINAGRVVPGYHAYLKRTPRTYQOREPAAHFPDYELFKLYS 389
 QY 379 QLYKIVPNVLEQGRKAKNPNDVAHSGVLLQYGMTEEMNYTVLFGVSRAIAGVLAQLI 438
 DB 390 TIVEAPGVCLFHGKTKNPNVNDHSGVLLQYGLTFASFTYLVGVAIRAIAGVLPOLI 449
 QY 439 SRALGFLEPKRSMTF---GLAKFVDSKS 465
 DB 450 DRAVGAPIERPKSFSTEKYKELVKKIESKN 479

RESULT 11

CISY_ARATH STANDARD; PRT: 473 AA.
 ID CISY_ARATH STANDARD; PRT: 473 AA.
 AC P20115; Q64869; Q8LE36; Q94EY6;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Citrate synthase, mitochondrial precursor (EC 2.3.3.1).
 GN ATG244350 OR F411.16.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91370823; PubMed=2491664;
 RT Unger E.A., Hand J.M., Cashmore A.R., Vasconcelos A.C.;
 RT "Isolation of a cDNA encoding mitochondrial citrate synthase from
 RL Arabidopsis thaliana.";
 RL Plant Mol. Biol. 13:411-418(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lih X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Cressy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Niernman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RIKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the
 RT SSP consortium (Salk/Stanford/GCFC).";
 RL Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R.,
 RA Feldmann K.;
 RT "Full-length cDNA from Arabidopsis thaliana.";
 RL Submitted (MAR-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate -> citrate +
 CC CoA.
 CC -1- PATHWAY: Tricarboxylic acid cycle.

CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CC CAPABLE OF OXIDATIVE METABOLISM.
 CC -1- SIMILARITY: Belongs to the citrate synthase family.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to frameshifts
 CC in positions 97; 105; 119; 125; 137; 149; 263; 271; 386; 390; 393;
 CC 398 and 403.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: X17528; CAA35570.1; ALT_FRAME.
 DR EMBL: AC004521; AAC16084.2; -
 DR EMBL: AF387018; AAK62463.1; -
 DR EMBL: AY085647; AAM62868.1; -
 DR HSSP: P23007; 2CSC
 DR Interpro: IPR002020; Citrate-synt.
 DR Pfam: PF00285; citrate_synt. 1.
 DR PRINTS: PR00143; CITRSTSNTASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
 KW Transferrase; tricarboxylic acid cycle; Mitochondrion; Transit peptide;
 KW Multigene family.
 FT CHAIN 1..16
 FT TRANSIT 1..16
 FT CHAIN 17..473
 FT ACT_SITE 307..307 CITRATE SYNTHASE.
 FT ACT_SITE 353..353 BY SIMILARITY.
 FT ACT_SITE 408..408 BY SIMILARITY.
 FT CONFLICT 17..17 V -> VO (IN REF. 1).
 FT CONFLICT 24..24 S -> N (IN REF. 4).
 FT CONFLICT 51..52 QQ -> HK (IN REF. 1).
 FT CONFLICT 111..111 V -> AL (IN REF. 1).
 FT CONFLICT 155..155 K -> S (IN REF. 1).
 FT CONFLICT 256..257 PV -> RL (IN REF. 1).
 FT CONFLICT 374..374 L -> H (IN REF. 1).
 FT CONFLICT 382..384 LVS -> CC (IN REF. 1).
 FT CONFLICT 447..449 ALG -> EL (IN REF. 1).
 FT CONFLICT 473..473 ALG -> EL (IN REF. 1).
 SO SEQUENCE 473 AA; 52654 MW; DF747D3DA8943FFB CRC64;

Query Match 61.5%; Score 1498.5; DB 1; Length 473;
 Best Local Similarity 62.6%; Pred. No. 3.5e-105;
 Matches 270; Conservative 77; Mismatches 83; Indels 1; Gaps 1;

QY 27 SASSTNLKDLIADLPKEDARIKTFROQHGKTVVQGLTVDMYGGMRGKGLVETSYLD 86
 DB 34 SSTDLKDSQGLPEQDRLKKSHEGKVOIGNITVDVIGMRCMTGLMETSLD 93
 QY 87 PDEGIRFGFSIPKQKLPKAKGGEPLPGCLVLTGHIPIEBQVSMISKAKAA 146
 DB 94 PEEGIRFGFSIPKQKLPKAKGGEPLPGCLVLTGHIPIEBQVSMISKAKAA 153
 QY 147 LPSHYTMDNPPTLHPMSQLSAVTPALNSESNFARAYAGISRTKRWELIYDSMLI 206
 DB 154 VPDVTYNAIDALPSTAHPTQFASGVMALOYSEFORAKENGHKSWEPTIEDCLWLI 213
 QY 207 AKLPCVAARIYRLYREGSGIGAIDSNLDMNSHFTNMLGYTDHOFTETRLYLTSHDHE 266
 DB 214 ARVPVAAYVYRMYKNGDSIPS -DKSLDYGANFSHMGFDEKVKELMRLYITSHDHE 272
 QY 267 GGNVSAHTSHLVGSALSDPYLSFAAAMNGIAGPLHGLANOEVWLTOLOKEVGKDVDE 326
 DB 273 GGNVSAHTSHLVGSALSDPYLSFAAAMNGIAGPLHGLANOEVWLTOLOKEVGKDVDE 332
 QY 327 KLRDVTNLTNSGRVVGXGAVLRTDPRYTCDDREFALHLPNDPMEKLYAOLYKIYPN 386
 DB 333 QLYKIVPNVLEQGRKAKNPNDVAHSGVLLQYGMTEEMNYTVLFGVSRAIAGVLPOLI 392
 QY 387 VLLDGGKAKNPNDVAHSGVLLQYGMTEEMNYTVLFGVSRAIAGVLPOLI 446

| | | | |
|--|---|---|---------|
| Db | | 393 VLTELGVKKNPWPVNDASHSVLLNHYGLTEARYTYVLFGVERSLGICQLLMDRALGLAL | 452 |
| Qy | 447 ERPKSMSTEG | 457 | |
| Db | 453 ERKPSVTMDWL | 463 | |
| RESULT 12 | | | |
| CISY_CANTR | STANDARD: | PRT: | 467 AA. |
| ID | CISY_CANTR | | |
| AC | P79024; | | |
| Dt | 01-NOV-1997 (Rel. 35, Created) | | |
| Dt | 01-NOV-1997 (Rel. 35, Last sequence update) | | |
| Dt | 15-SEP-2003 (Rel. 42, Last annotation update). | | |
| DE | Citrate synthase, mitochondrial precursor (EC 2.3.3.1). | | |
| CN | CIT. | | |
| OS | Candida tropicalis (Yeast). | | |
| OC | Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; | | |
| CC | Saccharomycetales; mitosporic Saccharomycetales; Candida. | | |
| CC | NCBI_TaxID=5482; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=ATCC 20336 / PK233; | | |
| RL | Ueda M., Sasaki S., Kawachi H., Shimizu K., Atomi H., Tanaka A.; | | |
| RA | Submitted (MAR-1997) to the EMBL/Genebank/DBJ databases. | | |
| CC | -1 CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate -> citrate + CoA. | | |
| CC | -1 PATHWAY: Tricarboxylic acid cycle. | | |
| CC | -1 SUBCELLULAR LOCATION: Mitochondrial matrix. | | |
| CC | -1 MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS CAPABLE OF OXIDATIVE METABOLISM. | | |
| CC | -1 SIMILARITY: Belongs to the citrate synthase family. | | |
| CC | ----- | | |
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| CC | ----- | | |
| DR | EMBL; AB001565; BAA19410.1; . | | |
| DR | HSSP; P23007; ZCSC. | | |
| DR | InterPro: IPR002020. Citrate_synth. | | |
| DR | Pfam; PF00285; citrate_synth_1. | | |
| DR | PRINTS; PR00143; CITRISTHASE. | | |
| DR | PROSITE; PS00480; CITRATE_SYNTHASE; 1. | | |
| KW | transferase; tricarboxylic acid cycle; Mitochondrion; Transalt peptide. | | |
| FT | TRANSIT 1 ? | | |
| FT | CHAIN ? | | |
| FT | ACT_SITE 301 301 | | |
| FT | ACT_SITE 347 347 | | |
| FT | ACT_SITE 402 | | |
| SO | SEQUENCE 467 AA; 52004 MM; 4B194132C4198CA2 CRC64; | | |
| Query Match 59.2%; Score 1442.5; DB 1; Length 467; Best local similarity 60.0%; Pred. No. 5,6e-101; Matches 269; Conservative 77; Mismatches 101; Indels 1; Gaps 1 | | | |
| Qy | 17 SCVLIAARHASASTNLIDLADLIIPKEQARIKTFRQHGKTVNGQITVDMMYGMRGMK | 76 | |
| Db | I : : : : I : : : : I : : : : I : : : : I : : : : I : : : : I : : : : I | | |
| Db | 16 STIKNSVRYTVTAEPFLTKORLEELIPAKAEVEVKOLKKDYGTVGIVELLEQAYGGMRGJK | 75 | |
| Qy | 77 GLAVETSVLDDEGRFSGFSIPEQOKLLPKRAGGEERLPESGFMLLYTGHTPTFEQYSW | 136 | |
| Db | I : : : : I : : : : I : : : : I : : : : I : : : : I : : : : I : : : : I | | |
| Db | 76 GLWVGCVSLDPIEGIRFERGRTIPDIQKELPKRPGGEEPLPALFMILLLTGEPTEAQTRA | 135 | |
| Qy | 137 LSKENAKRVADPPSHVVTLMDNFPTULAHMSOLSAAVTVLINSESNPARAYAOGISRTKYWE | 196 | |
| Db | I : : : : I : : : : I : : : : I : : : : I : : : : I : : : : I : : : : I | | |
| Db | 136 LSEEPFAANSALPKHNEELIDPSHLHHMAQFSIAVTLMDESQPAKAYAKGVHKSEYWK | 195 | |
| Qy | 197 LIYEDSDMLIAKLPCVAARKYIRNLIRBSGIGALDSINDWSHNFTNMGLGYTDH-OFTFLT | 255 | |

| | | | | | |
|-------------|--|--|-----------------------------------|--|--|
| Dd | 196 | VTYEDSDIELLAKFTIAKIKYRNFHDSKLPQAQIDSKDIDYANLANLSLGGPEENKEPELEM | 255 | | |
| Oy | 256 | RLYLTTHSDHGGGVNSAHTSHLVGSALSIDPLTSPRAAAMNGIAGVJHGLIANDVWLVTQL | 315 | | |
| Dd | 256 | RLYLTTHSDHGGGVNSAHTTHLVGSALSISPELSLAAGNGIAGVJHGRANDVEJEWLEFKL | 315 | | |
| Oy | 316 | OKEVGKDVSDCKLRDYIWNLTNSGRVYVGYHAVALRKDPHYTCORFALKHLPNDPMFK | 375 | | |
| Dd | 316 | REELNGDYSKAIEKYTLMDTILNAGRVGCGYHAVALRKDPHYTCORFALKHMDYELFK | 375 | | |
| Oy | 376 | LVAOLDYKIVPNVLLDQCKAKNPMPVNDASHGVLLDQYGMTEMYNYTVLFGVSRAGLVLAQ | 435 | | |
| Dd | 376 | LVSNIVYEAPVGFVPOHGMKTKMPMPNVGSHSGSVLLDQYGLTDESEFTVLFVGSRAFGVLQ | 435 | | |
| Oy | 436 | LWMSRAGLEPLERPKSMSTEDLMFVDS | 463 | | |
| Dd | 436 | LILDRGLGMPLEPKSESTERYIELVNS | 463 | | |
| RESULT 13 | | | | | |
| ID | CISY_CITMA | STANDARD: | PRT: 471 AA. | | |
| AC | P49298: | | | | |
| Dt | 01-FEB-1996 | (Rel. 33, Created) | | | |
| Dt | 01-FEB-1996 | (Rel. 33, Last sequence update) | | | |
| Dt | 15-SEP-2003 | (Rel. 42, Last annotation update) | | | |
| DE | Citrate synthase, mitochondrial precursor (EC 2.3.3.1). | | | | |
| GN | CIT | | | | |
| OS | Citrus maxima (Pummelo) (Citrus grandis). | | | | |
| OC | Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | |
| OC | Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; | | | | |
| OX | eucosids II; Sapindales; Rutaceae; Citrus. | | | | |
| OX | NCBI_TaxID=37334; | | | | |
| RA | [1] | | | | |
| RC | SEQUENCE FROM N.A. | | | | |
| RL | STRAIN=cv. Siamese Sweet 2240; | | | | |
| RL | Canel C.; | | | | |
| CC | Theis (1994), University of California / Riverside, U.S.A. | | | | |
| CC | -1- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate = citrate + CoA. | | | | |
| CC | -1- PATHWAY: Tricarboxylic acid cycle. | | | | |
| CC | -1- SUBUNIT: Homodimer (By similarity). | | | | |
| CC | -1- SUBCELLULAR LOCATION: mitochondrial matrix. | | | | |
| CC | -1- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS | | | | |
| CC | CAPABLE OF OXIDATIVE METABOLISM. | | | | |
| CC | -1- SIMILARITY: Belongs to the citrate synthase family. | | | | |
| CC | ----- | | | | |
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| CC | entities requires a license agreement (see http://www.isb-sib.ch/announce/ | | | | |
| CC | or send an email to license@isb-sib.ch). | | | | |
| CC | ----- | | | | |
| DR | EMBL: U19481: AAB82743.1; - | | | | |
| DR | HSSP: P23007: 2CSC | | | | |
| DR | InterPro: IPR002020: Citrate_synth. | | | | |
| DR | Pfam: PF00285: citrate_synth.1 | | | | |
| DR | PRINTS: PR00143: CITRITSNTHASE. | | | | |
| DR | PROSITE: PS00480: CITRATE_SYNTHASE; 1. | | | | |
| KM | Transferrase; Tricarboxylic acid cycle; Mitochondrion; Transit peptide. | | | | |
| FT | TRANSIT | 1 | 18 | | |
| FT | CHAIN | 19 | 471 | | |
| FT | ACT_SITE | 307 | 307 | | |
| FT | ACT_SITE | 353 | 353 | | |
| FT | ACT_SITE | 408 | 408 | | |
| FT | SEQUENCE | 471 AA; | 52183 MM; | | |
| Query Match | Best Local Similarity | 58.9%; | Score 1435.5; DB 1; Length 471; | | |
| Matches | 269; Conservative | 80; | Mismatches 105; Indels 5; Gaps 2; | | |

QY 5 TAAALLG-----TKNASCLVLAARHASSTNLKDLADLLPEQOARIKTERFOHQKTVV 60
 DB 8 TALSRLSRAGQSNLSNSVRMLQMOSSADLDHLSQLEKEMPEQOERLKVKVSDGKROL 67
 QY 61 GQIVDMYVGMGRKKGKGLVETSVLDPEDEIRFGFSIPECOKLLPKAKGEEPLPEGLF 120
 DB 68 GNITDVIYGGKMGKMTGLMETSILDPDEGIRFRNLSIPECOKLLPKAKPDEPLPEGL 127
 QY 121 WLVYGHIPTEBOVWMLSKENAKRALPSHVYTMNDPNTLHPMSQLSAAVTAALNSNSN 180
 DB 128 WLLLGKVPKSEQVDGLSKELDRATVPDYKALDALPVAHPMTOFASGVMAQVOSE 187
 QY 181 FARVAQGISRTKYWELIYEDSMDLIAKPCVAKIYNNLYREGSGAIDSNLDMSHNF 240
 DB 188 FOEAVEKGIHKSKEPTSEDSNLIAVPVAAYVQRIYKDGKILIRK-DDSLDYGNF 246
 QY 241 TNNMGTYDHOETELRLTLTTHSDHEGCVNSAHTSHLYGSALSDPYLSPFAAAMGLAPL 300
 DB 247 SHMLGFDDPKMLELRLVYTHSHDEGCVNSAHTGHVLAASALSDPYLSPFAAAMGLAPL 306
 QY 301 HGLAQEVLVMTLOKEVGVKDSDEKLADYTMNTLNSGRVVPYGVHVAIRKTDPRYCO 360
 DB 307 HGLAQEVLVMTKSVYDDEGCVNTTBOQLKDYVMKTLNSGKVPYGVHVAIRKTDPRYCO 366
 QY 361 REFALKHLPPNPMFRLVAQLKYVNVLLBOGKAKNPVNDASHGVLLQYVGMTEMYV 420
 DB 367 REFALKHLPPDPLPOLVSKLEVVPPIITLKGKVNPNPNDAHSGVLLNHGGLAEARY 426
 QY 421 TVLEFVSRAVLAQVLAQVLSRALGFLERPKSMSTEGMLK 459
 DB 427 TVLEFVSRSLSIGSOLIMDRALGLPLERPKSVTLDMIEK 465

RESULT 14

CITS2_YEAST STANDARD: PRT: 460 AA.
 AC P08679;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Citrate synthase, peroxisomal (EC 2.3.3.1).
 GN C172 OR YCR005C OR YCR5C OR YCR043.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92254505; PubMed=1580102;
 RA Bileau N., Fremaux C., Hebrard S., Menara A., Aigle M., Crouzet M.;
 RT "The complete sequence of a 10.8kb fragment to the right of the
 RT chromosome III centromere of Saccharomyces cerevisiae.";
 RL Yeast 8:61-70(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87089811; PubMed=3540614;
 RA Rosenkrantz M., Alam T., Kim K.-S., Clark B.J., Stere P.A.,
 RA Guarente L.P.;
 RT "Mitochondrial and nonmitochondrial citrate synthases in
 RT Saccharomyces cerevisiae are encoded by distinct homologous genes.";
 RL Mol. Cell. Biol. 6:4509-4515(1986).
 RN [3]
 RP SEQUENCE OF 1-24 FROM N.A.
 RX MEDLINE=91094853; PubMed=1986232;
 RA Liao X., Small W.C., Stere P.A., Butow R.A.;
 RT "Intramitochondrial functions regulate nonmitochondrial citrate
 RT synthase (C172) expression in Saccharomyces cerevisiae.";
 RL Mol. Cell. Biol. 11:38-46(1991).
 CC -I- CATALYTIC ACTIVITY: Acetyl-CoA + H(2)O + oxaloacetate -> citrate +
 CC CoA.
 CC -I- PATHWAY: Tricarboxylic acid cycle.
 CC -I- SUBCELLULAR LOCATION: Peroxisomal.

CC -I- MISCELLANEOUS: CITRATE SYNTHASE IS FOUND IN NEARLY ALL CELLS
 CC CAPABLE OF OXIDATIVE METABOLISM.
 CC -I- SIMILARITY: Belongs to the citrate synthase family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sib-sib.ch).
 CC -----

DR EMBL: Z11113; CAAT7442.1;
 DR EMBL: M14686; AAA34497.1;
 DR EMBL: M54982; AAA34498.1;
 DR EMBL: X59720; CAA42342.1;
 DR PIR: A25393; YKBYC.
 DR HSSP: P23007; ZCSC.
 DR SGD: S0000598; C172.
 DR GO: GO:0005777; C:peroxisome; IDA.
 DR InterPro: IPR002020; Citrate_synth.
 DR Pfam: PF00285; citrate_synth.
 DR PRINTS: PR00143; CITRATESNHASE.
 DR PROSITE: PS00480; CITRATE_SYNTHASE; 1.
 KW transferase; tricarboxylic acid cycle; peroxisome; Multigene family.
 FT ACT_SITE 293 293 BY SIMILARITY.
 FT ACT_SITE 339 339 BY SIMILARITY.
 FT ACT_SITE 394 394 BY SIMILARITY.
 FT SITE 458 460 MICROBODY TARGETING SIGNAL (POTENTIAL).
 SQ SEQUENCE 460 AA: 51413 MW; AB2F6AD9A9399EF CRC64;

Query Match 58.5%; Score 1425; DB 1; Length 460;
 Best Local Similarity 59.9%; Pred. No. 1.le-99;
 Matches 264; conservative 72; Mismatches 101; Indels 4; Gaps 2;

QY 27 SASSTNLKDLADLLPEQOARIKTERFOHQKTVVGGITVDMYVGMGRKGLVETSVLD 86
 DB 20 SSOEKLTERKERESEIPIHAODVROFVKHGHKTKISDVLLQVYGGMRGIPESVWEGSYLD 79
 QY 87 PDEGIRFGFSIPECOKLLPKAKGEEPLPEGLTFLVYGHIPREOVSWLSKEAKRAA 146
 DB 80 PEDGIRFGKRTIADIQKLPKAKGSSQPLPEALVLLTGEVPTQAVENLSADIMRSSE 139
 QY 147 LPSHVYTMNDPNTLHPMSQLSAAVTAALNSNSNFARVAQGISRTKYWELIYEDSDMLI 206
 DB 140 LPSHVYTMNDPNTLHPMSQLSAAVTAALNSNSNFARVAQGISRTKYWELIYEDSDMLI 199
 QY 207 AKLPCVAKIYNNLYREGSGAIDSNLDMSHNFMTNLGYTDHOETELRLTLTHSDHE 266
 DB 200 GKLPIYIAKIRYNNVFKDK-MGEVDPNADYAKNLVNLIGSDEDEVDLMRLYLTTHSDHE 258
 QY 267 GGNVAHSHLYVGSALSDPYLSPFAAAMGLAGPLHGLANOEVLVMTLOKEVGVKDSDE 326
 DB 259 GGNVAHSHLYVGSALSDPYLSPFAAAMGLAGPLHGLANOEVLVMTLOKEVGVKDSDE 318
 QY 327 KLADYTMNTLNSGRVVPYGVHVAIRKTDPRYCOREFALKHLPPNPMFRLVAQLKYVNP 386
 DB 319 TIEKLMPTLNSGRVVPYGVHVAIRKTDPRYCOREFALKHLPPNPMFRLVAQLKYVNP 378
 QY 387 VLEEGKAKNPVNDASHGVLLQYVGMTEMYVTVLEFVSRAVLAQVLAQVLSRALGFL 446
 DB 379 VLEHGKTKNPNPNDAHSGVLLQYVGMTEMYVTVLEFVSRAVLAQVLAQVLSRALGFL 438
 QY 447 ERPKSMSTEGMLK 464
 DB 439 ERPKSYSTEKKYELKNIESK 459

RESULT 15

CITSY_FRAAN STANDARD: PRT: 469 AA.
 AC P83572;
 DT 28-FEB-2003 (Rel. 41, Created)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 5, 2003, 20:07:47; Search time 42 seconds
(without alignments)
1067.014 Million cell updates/sec

Title: US-09-996-223-1

Perfect score: 2436
Sequence: 1 MALTTAAARLGTCKNASCIV.....ERKSKSTEGLMKRVDSKSG 466

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------------|
| 1 | 2339 | 96.0 | 464 | 1 | YKRG citrate (sl)-synth |
| 2 | 1693 | 69.5 | 468 | 2 | S42370 citrate (sl)-synth |
| 3 | 1519 | 62.4 | 473 | 2 | T39028 citrate synthase P |
| 4 | 1501.5 | 61.6 | 469 | 2 | T49379 citrate synthase |
| 5 | 1498.5 | 61.6 | 479 | 1 | YKBY citrate (sl)-synth |
| 6 | 1498.5 | 61.5 | 474 | 2 | T02390 citrate (sl)-synth |
| 7 | 1495.5 | 61.4 | 469 | 2 | S41563 citrate (sl)-synth |
| 8 | 1473.5 | 60.5 | 433 | 2 | T47834 citrate synthase-1 |
| 9 | 1425 | 58.5 | 460 | 1 | YKBYC citrate (sl)-synth |
| 10 | 1349 | 55.4 | 471 | 2 | S44316 citrate (sl)-synth |
| 11 | 1219 | 50.0 | 462 | 2 | UC5625 14-nm filament pro |
| 12 | 1157.5 | 47.5 | 472 | 1 | YKMW citrate (sl)-synth |
| 13 | 1108.5 | 45.5 | 339 | 2 | T09334 citrate (sl)-synth |
| 14 | 1063.5 | 43.7 | 486 | 2 | S52814 citrate (sl)-synth |
| 15 | 356 | 14.6 | 437 | 2 | I40717 citrate (sl)-synth |
| 16 | 351 | 14.4 | 436 | 1 | YKOPC citrate (sl)-synth |
| 17 | 346 | 14.2 | 397 | 2 | S74344 citrate synthase 9 |
| 18 | 345.5 | 14.2 | 427 | 2 | B81139 citrate synthase |
| 19 | 339.5 | 13.9 | 514 | 2 | T49158 citrate synthase-1 |
| 20 | 338 | 13.9 | 428 | 1 | YKPSCA citrate (sl)-synth |
| 21 | 338 | 13.9 | 428 | 1 | B83448 citrate synthase P |
| 22 | 338 | 13.9 | 509 | 2 | C84858 citrate synthase |
| 23 | 332.5 | 13.6 | 431 | 2 | E70782 citrate synthase |
| 24 | 331.5 | 13.6 | 431 | 2 | T45353 citrate synthase |
| 25 | 327.5 | 13.4 | 430 | 2 | J01392 citrate (sl)-synth |
| 26 | 327.5 | 13.4 | 435 | 2 | D97863 citrate synthase |
| 27 | 324.5 | 13.3 | 411 | 2 | A75479 citrate synthase |
| 28 | 324 | 13.3 | 426 | 2 | B87485 citrate synthase |
| 29 | 322.5 | 13.2 | 372 | 2 | B84044 citrate synthase |

| | | | | | |
|----|-------|------|-----|---|---------------------------|
| 30 | 322.5 | 13.2 | 516 | 2 | S53007 citrate synthase |
| 31 | 320 | 13.1 | 441 | 2 | P86708 citrate (sl)-synth |
| 32 | 318 | 13.1 | 378 | 2 | AF1854 citrate synthase |
| 33 | 315.5 | 13.0 | 427 | 1 | YKEC citrate (sl)-synth |
| 34 | 315.5 | 13.0 | 427 | 2 | A99722 citrate synthase |
| 35 | 315 | 12.9 | 437 | 2 | AF3356 citrate (sl)-synth |
| 36 | 314 | 12.9 | 424 | 2 | I39506 citrate (sl)-synth |
| 37 | 313 | 12.8 | 429 | 2 | D82669 citrate synthase X |
| 38 | 311.5 | 12.8 | 436 | 1 | YKRECP citrate synthase |
| 39 | 309.5 | 12.7 | 427 | 2 | H85572 citrate synthase V |
| 40 | 309 | 12.6 | 431 | 2 | B82119 citrate synthase |
| 41 | 307.5 | 12.6 | 431 | 2 | I40044 citrate (sl)-synth |
| 42 | 304 | 12.5 | 429 | 2 | AH2747 citrate synthase |
| 43 | 304 | 12.5 | 429 | 2 | C97528 citrate synthase |
| 44 | 303.5 | 12.5 | 367 | 2 | B72394 citrate synthase |
| 45 | 303.5 | 12.5 | 427 | 2 | AF0590 citrate synthase |

ALIGNMENTS

RESULT 1

YKRG citrate (sl)-synthase (EC 4.1.3.7) precursor - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 15-Oct-1982 #sequence_revision 30-Sep-1992 #text_change 05-May-2000

C:Accession: A29966; A01109; A61347

R:Evans, C.T.; Owens, D.D.; Sumegi, B.; Kispal, G.; Stree, P.A.

Biochemistry 27, 4680-4686, 1988

A:Title: Isolation, nucleotide sequence, and expression of a cDNA encoding pig citre

A:Reference number: A29966; MUID:89000665; PMID:3048387

A:Accession: A29966

A:Molecule type: mRNA

A:Residues: 1-464 <EVA>

R:BioRxham, D.P.; Parmelee, D.C.; Kumar, S.; Walsby, K.A.; Tilani, K.

Biochemistry 21, 2028-2036, 1982

A:Title: Complete amino acid sequence of porcine heart citrate synthase:

A:Reference number: A90457; MUID:82231993; PMID:7093227

A:Accession: A01109

A:Molecule type: protein

A:Residues: 28-464 <BL0>

R:BioRxham, D.P.; Parmelee, D.C.; Kumar, S.; Walsby, K.A.; Tilani, K.

Proc. Natl. Acad. Sci. U.S.A. 78, 5381-5385, 1981

A:Title: Primary structure of porcine heart citrate synthase.

A:Reference number: A61347; MUID:82060250; PMID:6795032

A:Accession: A61347

A:Molecule type: Protein

A:Residues: 28-464 <BL2>

R:Remington, S.; Wiegand, G.; Huber, R.

J. Mol. Biol. 158, 111-152, 1982

A:Title: Crystallographic refinement and atomic models of two different forms of cit

A:Reference number: A92884; MUID:83010291; PMID:7120407

A:Contents: annotation; X-ray crystallography, 2.7 and 1.7 angstroms

A:Comment: Citrate (sl)-synthase is found in nearly all cells capable of oxidative r

cycle.

C:Comment: It is synthesized in the cytoplasm but functions in the mitochondrion of

C:Comment: This molecule is a dimer of identical chains. Each dimer binds two molec

C:Superfamily: citrate (sl)-synthase

C:Keywords: carbon-carbon lyase; coenzyme A; homodimer; methylated amino acid; mitoc

F:1-27/Domain: transit peptide (mitochondrion) #status predicted <SIG>

F:28-464/Product: citrate (sl)-synthase #status experimental <MNT>

F:301-347/402/Active site: His, His, Asp #status predicted

F:395/Modified site: N6,N6,N6-trimethyllysine (Lys) #status experimental

Query Match 96.0%; Score 2339; DB 1; Length 464;

Best Local Similarity 96.1%; Pred. No. 5,8e-169;

Matches 446; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MALTTAAARLGTCKNASCIVLAARHSAASSTNKDILADLPEORARITFRROHKTAV 60

Db 1 MALTTAAARLGTCKNASCIVLAARHSAASSTNKDILADLPEORARITFRROHKTAV 60

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QY 61 GQITVDMMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPEGLF 120
 DB 61 GQITVDMMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPEGLF 120
 QY 121 WLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 180
 DB 121 WLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 180
 QY 181 FARAAAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 240
 DB 181 FARAAAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 240
 QY 241 TMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGLAGPL 300
 DB 241 TMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGLAGPL 300
 QY 301 HGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPRYTCQ 360
 DB 301 HGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPRYTCQ 360
 QY 361 REFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGMEEMNY 420
 DB 361 REFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGMEEMNY 420
 QY 421 TVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 464
 DB 421 TVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 464

RESULT 2

S42370
 citrate (si)-synthase (EC 4.1.3.7) precursor - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C>Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #extl_change 05-May-2000
 C:Accession: S42370
 R:Smith, A.
 submitted to the EMBL Data Library, March 1994
 A:Reference number: S42368
 A:Accession: S42370
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-466 <SMI>
 A:Cross-references: EMBL:230423; NID:9458479; PID:9458482
 C:Genetics:
 A:Introns: 69/3; 202/3; 309/3
 C:Superfamily: citrate (si)-synthase
 C:Keywords: carbon-carbon lyase; coenzyme A; mitochondrion; oxo-acid-lyase

Query Match 69.5%; Score 1693; DB 2; Length 466;

Best Local Similarity 68.3%; Pred. No. 3.9e-120;

Matches 315; Conservative 62; Mismatches 82; Indels 2; Gaps 1;

QY 1 MALLTAAARLLGTRKN--SCLVLAARHSAASSTNLKDIADLPKBEAKRTTROOHGKT 58
 DB 1 MALLTAAARLLGTRKN--SCLVLAARHSAASSTNLKDIADLPKBEAKRTTROOHGKT 58
 QY 59 VVGQITVDMMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPEGS 118
 DB 59 VVGQITVDMMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPEGS 118
 QY 61 VVGNVNNDIMLYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPEGA 120
 DB 61 VVGNVNNDIMLYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPEGA 120
 QY 119 LFWLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 178
 DB 119 LFWLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 178
 QY 121 IMWLLTGVDPSEAKQTAAITKENNARADLPTHVVRMDNPPDNLHPMAQETIAIAALNNE 180
 DB 121 IMWLLTGVDPSEAKQTAAITKENNARADLPTHVVRMDNPPDNLHPMAQETIAIAALNNE 180
 QY 179 SNFRARAYAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 238
 DB 179 SNFRARAYAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 238
 QY 181 SKFGAARAYAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 240
 DB 181 SKFGAARAYAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 240
 QY 239 NFWTMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGLAG 298
 DB 239 NFWTMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGLAG 298
 QY 241 NFWTMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGLAG 300
 DB 241 NFWTMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGLAG 300
 QY 299 PLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPRYT 358
 DB 299 PLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPRYT 358

DB 301 PLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPRYT 360
 QY 359 COREFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGMEEMNY 418
 DB 359 COREFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGMEEMNY 418
 QY 419 YTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 459
 DB 419 YTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 459

RESULT 3

T39028
 citrate synthase precursor, mitochondrial - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #extl_change 21-Jan-2000
 C:Accession: T39028
 R:Devlin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, February 1996
 A:Reference number: 221750
 A:Accession: T39028
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-473 <DEV>
 A:Cross-references: EMBL:269731; PID:CAA93617.2; GSPDB:GN00066; SPDB:SPAC6C3.04
 A:Experimental source: strain 972h-; cosmid c6C3
 C:Genetics:
 A:Gene: SPAC6C3.04
 A:Map position: 1
 A:Genome: nuclear
 C:Superfamily: citrate (si)-synthase
 C:Keywords: mitochondrion

Query Match 62.4%; Score 1519; DB 2; Length 473;

Best Local Similarity 61.3%; Pred. No. 5.6e-107;

Matches 287; Conservative 75; Mismatches 96; Indels 10; Gaps 3;

QY 6 AARLLGTRKNASCLVLAARH-----SASSTNLKDIADLPKBEAKRTTROOHGKT 57
 DB 6 AARLLGTRKNASCLVLAARH-----SASSTNLKDIADLPKBEAKRTTROOHGKT 57
 QY 7 ASTRIASSTLSLSOASLRKROLNPLFTSSYSTRSSSLDRALPEKQALTKKRAEHGQ 66
 DB 7 ASTRIASSTLSLSOASLRKROLNPLFTSSYSTRSSSLDRALPEKQALTKKRAEHGQ 66
 QY 58 TVVGOITVDMMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPE 117
 DB 58 TVVGOITVDMMYGGMRGKGLVETSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPE 117
 QY 67 DVIGEVITNOMYGAGKRVSLIMEGSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPE 126
 DB 67 DVIGEVITNOMYGAGKRVSLIMEGSVLDPDEGIRFRGFSIPECOKLLPKRKGEEPLPE 126
 QY 118 GLFWLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 177
 DB 118 GLFWLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 177
 QY 127 SLFWLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 186
 DB 127 SLFWLLVTGHIPTBEQVSWLSKEMAKRALPSSHVYTMNDNPTNLHPMSQLSAAVYALNSEN 186
 QY 178 SNFRARAYAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 237
 DB 178 SNFRARAYAGISIRTKYVELLYEDSMOILAKPCVAATYRNLYREGSGICAIIDNSMDMNF 237
 QY 187 DSFAKAYERKGNKNDKYETEDMDIATVPIAGIITRNLYREGSGICAIIDNSMDMNF 245
 DB 187 DSFAKAYERKGNKNDKYETEDMDIATVPIAGIITRNLYREGSGICAIIDNSMDMNF 245
 QY 238 NFWTMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGL 296
 DB 238 NFWTMMGLGYTHQFETRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGL 296
 QY 246 YVFAVAVLGFANNEEVELMRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGL 305
 DB 246 YVFAVAVLGFANNEEVELMRLTYLTTHSDHEGNSAHTSHLVGALSALDPTLSFAAAMNGL 305
 QY 297 AGPLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPR 356
 DB 297 AGPLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPR 356
 QY 306 AGPLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPR 365
 DB 306 AGPLHGLANQEVLMVLTOLQEKVGVDSDEKLDYIMNTLNSGRVVPYGHAVLKRKTDPR 365
 QY 357 YTCQREFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGME 416
 DB 357 YTCQREFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGME 416
 QY 366 YTAQREFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGME 425
 DB 366 YTAQREFALKHLPNDPMFKLVNOLQKIVPNVLEOGKAKNPMPNVDAHSGVLLQYTGME 425
 QY 417 NMYTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 464
 DB 417 NMYTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 464
 QY 426 QSFYTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 473
 DB 426 QSFYTVLFGVSRALGVLAOLIMSRALGFPLERPKSMSTEGIMKFFVDSK 473

RESULT 4

T49379

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